

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus.p2n model

Run on: June 26, 2006, 19:42:38 ; Search time 5782 Seconds
(without alignments)
3964.917 Million cell updates/sec

Title: US-10-817-483-2

Perfect score: 1230
Sequence: 1 MDLRILFGPTCTGKTSTAIA.....KPLVGAFAVEAFEGPPFRM 239

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 636136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match length DB ID Description

1 1230 100.0 1919 2 CQ895587 X1410 Agrobacteri
2 1230 100.0 1919 15 ABTITPT AK039930 Sequence
3 1230 100.0 2722 2 AK039930 Sequence

4 1230 100.0 2722 2 AX039931 AX039931 Sequence
5 1230 100.0 3017 2 AX039934 AX039934 Sequence
6 1230 100.0 5622 2 AX039929 AX039929 Sequence
7 1075 87.4 723 2 CQ899250 CQ899250 Sequence
8 1075 87.4 1983 15 ATTMPTI X00639 Agrobacteri
9 1075 87.4 9931 15 AE007927 AE007927 Agrobacte
10 1075 87.4 10377 15 AE009419 AE009419 Agrobacte
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12 1066 86.7 29524 15 AB025109 AB025109 Agrobacte
13 1052 85.5 1997 15 AB025109 AB025109 Agrobacte
14 1050 85.4 1382 15 PLATIPG X17428 Plasmid Ti
15 1050 85.4 10200 15 ATTAAAH X56185 A. tumefaci
16 1050 85.4 14960 15 AVU83986 AVU83986 Agrobacteri
17 1050 85.4 15463 15 AVU83987 AVU83987 Agrobacteri
18 1035 84.1 2724 15 AB032122 AB032122 Agrobacte
19 1005 81.7 723 2 AR564460 AR564460 Sequence
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21 1005 81.7 1988 15 ATTMR X00010 Agrobacteri
22 1005 81.7 24595 2 BD016312 BD016312 Method of
23 1005 81.7 24595 2 E00404 E00404 Ti Plasmid
24 1005 81.7 24595 2 E00546 E00546 DNA fragment
25 1005 81.7 24595 2 AR364803 AR364803 Sequence
26 1005 81.7 24595 15 ATACHS X00493 Agrobacteri
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29 994 80.8 747 2 AR564455 AR564455 Sequence
30 993 80.7 6482 15 AVIAAM X73327 A. vitis 1aa
31 984 80.0 3183 2 I75096 I75096 Sequence 1
32 686.5 55.8 2544 2 AR564457 AR564457 Sequence
33 614 48.9 3271 15 TS4RPTV M91610 Plasmid PTi
34 610.5 49.6 813 15 ARTZSG X16380 Agrobacteri
35 605.5 49.2 1413 15 ATTZS X02423 Agrobacteri
36 605.5 49.2 206479 15 AB016260 AB016260 Agrobacte
37 604.5 49.1 1403 2 I05195 I05195 Sequence 1
38 603.5 49.1 1403 15 ATTZS1 X03933 Agrobacteri
39 603.5 49.1 2171 15 AE007942 AE007942 Agrobacte
40 603.5 49.1 10165 15 AE009435 AE009435 Agrobacte
41 603.5 49.1 29802 15 TTPREGU AB039932 Agrobacte
42 600.5 48.8 73934 15 AB039932 Agrobacte
43 600.5 48.8 217594 15 AP002086 AP002086 Agrobacte
44 557 48.3 584 2 I18499 I18499 Sequence 2
45 542.5 44.1 110000 15 AE013598_31 Continuation (32 o

ALIGNMENTS

RESULT 1
LOCUS CQ895587 1919 bp DNA linear PAT 05-NOV-2004
DEFINITION Sequence 1 from Patent WO2004090143.
ACCESSION CQ895587
VERSION CQ895587.1 GI:55467720
KEYWORDS
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE 1
AUTHORS Habben, J.F., Zinselmeier, C., Tomez, D.T., Abdlit, S.E.,
Helentjaris, T.G. and Niu, X.
TITLE Modulation of cytokinin activity in plants
JOURNAL Patent: WO 2004090143-A 1 21-OCT-2004;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source
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690..1409
/note="unnamed protein product; ipt"
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/protein_id="CAH6599.1"

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ORIGIN

Alignment Scores:

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|------------------------|-----------|---------------|------|
| Pred. No.: | 1,976-126 | Length: | 1919 |
| Score: | 1230.00 | Matches: | 239 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-10-817-483-2 (1-239) x CO895587 (1-1919)

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DB 690 ATGGATCTACGCTTAATTTTGGTCCAACTGGCACAGAAAGACATCGACGTGACT 749
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 750 CTGGCCACGACAGACTGGCTCCAGTCTCTCGCTCGATCGGTCGAATGCTGCTCA 809
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyThrThrArgLeuTyr 60
DB 810 CTATCAACCGGAAAGCGGCGACCAACAGTGAAGAAGAAAGAAACACACTCGTCTGAC 869
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu 80
DB 870 CTGTATGATCCGCTTTGGTAAAGGATATCATTTACGCCAACCACTCATAGAACGGCTC 929
QY 81 IleAlaGlnValHisAsnHisGlnValAlaLysGlyLeuIleLeuGlnGlyGlySerIle 100
DB 930 ATTGGGAGGTGCAACATCACAGAGCCAAAGCGGCTTATTTCTTGAAGGAGATCTATC 989
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
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QY 121 IleArgAsnGlnLeuAlaAspGlnGlnSerPheMetSerValAlaLysThrArgValLys 140
DB 1050 ATTGCGAACGAGTTGCGACAGAGAGCTTCATGACGCTGCGCCAAACCGAGTTAAG 1109
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DB 1110 CAGATGTTACGCCCTCTGACAGGTCTTCTATTATCCAAAGATTGGTCAACTTGGAGG 1169
QY 161 GluProAlaGlnLeuArgProIleLeuGlnGlnIleAspGlyTyrTrpArgTyrAlaLeuLeuPhe 180
DB 1170 GAGCTTCGCGTGAAGCCCATCTGAGAGGAGATCGATGATATCGATATGCCCTGTATT 1229
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
DB 1230 GCTACCCGAAACAGATACGCCCGCATATGCTATTGCGAGCTCGACGCGATATGAGAAAT 1289
QY 201 LysLeuIleHisGlyIleAlaGlnGlnLeuLeuIleHisAlaArgArgGlnGlnGlnLys 220
DB 1290 AAATGATTCACAGGATACGCTCAGAGATTCTTAATCCATGCGCGTCGACAGGAACAGAA 1349
QY 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlnGlyProProPheArgMet 239
DB 1350 TTCCCTTTGTGGGCGACAGCTGTTCAGAGCGTTTGAAGACCACTTTCGATG 1406

RESULT 2

ABTIPT 1919 bp DNA linear BCT 12-SEP-1993
LOCUS Agrobacterium tumefaciens Ti plasmid ipt gene for isopenentenyl
DEFINITION
ACCESSION X14410.1 GI:38689
VERSION X14410.1 GI:38689

KEYWORDS

ipt gene; isopenentenyl transferase; transferase.
Agrobacterium tumefaciens (Rhizobium radiobacter)

SOURCE

Agrobacterium tumefaciens

ORGANISM

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

REFERENCE

Rhizobiaceae; Agrobacterium.

AUTHORS

1 (bases 1 to 1919)

TITLE

Strabala, T.J., Bednarek, S.Y., Bertoni, G., and Amsino, R.M.

JOURNAL

Isolation and characterization of an ipt gene from the Ti plasmid

PUBMED

B0542

AUTHORS

Mol. Gen. Genet. 216 (2-3), 388-394 (1989)

TITLE

2747621

PUBMED

2 (bases 1 to 1919)

AUTHORS

Strabala, T.

TITLE

Direct Submission

JOURNAL

Submitted (02-FEB-1989) Strabala T., Department of Biochemistry,
University of Wisconsin Madison, 420 Henry Mall, Madison WI 53706

FEATURES

Location/Qualifiers

source

1..1919

CDS

/organism="Agrobacterium tumefaciens"
/mol_type="genomic DNA"
/strain="B0542"
/db_xref="taxon:358"
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/plasmid="Ti"
690..1409
/note="unnamed protein product; isopenentenyl transferase
(AA 1-239)"
/codon_start=1
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/protein_id="CAA32582.1"
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/db_xref="GOA:P15653"
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ORIGIN

Alignment Scores:

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|------------------------|-----------|---------------|------|
| Pred. No.: | 1,976-126 | Length: | 1919 |
| Score: | 1230.00 | Matches: | 239 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 15 | Gaps: | 0 |

US-10-817-483-2 (1-239) x ABTIPT (1-1919)

QY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 690 ATGGATCTACGCTTAATTTTGGTCCAACTGGCACAGAAAGACATCGACGTGACT 749
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 750 CTGGCCACGACAGACTGGCTCCAGTCTCTCGCTCGATCGGTCGAATGCTGCTCA 809
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyThrThrArgLeuTyr 60
DB 810 CTATCAACCGGAAAGCGGCGACCAACAGTGAAGAAGAAAGAAACACACTCGTCTGAC 869
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu 80
DB 870 CTGTATGATCCGCTTTGGTAAAGGATATCATTTACGCCAACCAAGCTCATGAACGGCTC 929
QY 81 IleAlaGlnValHisAsnHisGlnValAlaLysGlyLeuIleLeuGlnGlyGlySerIle 100
DB 930 ATTGGGAGGTGCAACATCACAGAGCCAAAGCGGCTTATTTCTTGAAGGAGATCTATC 989
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 990 TCGTTGCTCAGAGTGCATGCGCAAGTCGTTATTGGAACCGGATTTTCGTGGCATATT 1049

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| QY | 121 | lleargaengluleuAlaaspGluserPheMetSerValAlaIyThrArgValIys | 140 |
| Db | 1050 | ATTGCCAACGAGTTAGCAGACGAGAGAGCTTCAATGACCGCGCCAAACACAGAGTTAAAG | 1109 |
| QY | 141 | GlnMetLeuArgProSerAlaGlyLeuSerLeileIeGlnGluLeuValGlnLeuThrArg | 160 |
| Db | 1110 | CAGATGTTACGCCCTCTGCAGAGTCTTCTATTATCAAGAGTTGGTTCAACTTTGGAGG | 1169 |
| QY | 161 | GluProArgLeuArgProIleuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe | 180 |
| Db | 1170 | GAGCTCGGCTGAGGCCCATCTGSAAGGATCGATGSAATTCGATAGCCCTGCTATT | 1229 |
| QY | 181 | AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn | 200 |
| Db | 1230 | GCTACCCGAAACAGATCAGCCCGATATGCTATTGCGAGCTCGACGCGAGATATGGAAGAT | 1289 |
| QY | 201 | LysLeuLeileIeIleGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnLys | 220 |
| Db | 1290 | AAATTGATTCCACGGTATCGCTCAGAGATTCTTAATCCATGCGCGTCGACAGAAACAGAAA | 1349 |
| QY | 221 | PheProLeuValGlyAlaAlaThrAlaValGlnIaPheGlnGlyProProPheArgMet | 239 |
| Db | 1350 | TTCCCTTTGGTGGGGCGACAGCTGTGCAAGCGTTTGAAGACCACTTTTCGATG | 1406 |

| LOCUS | AX039930 | 2722 bp | DNA | linear | PAT 18-NOV-2000 |
|------------|--|-------------|-----|--------|-----------------|
| DEFINITION | Sequence 8 from Patent WO0063401. | | | | |
| ACCESSION | AX039930 | | | | |
| VERSION | AX039930.1 | GI:11229959 | | | |
| KEYWORDS | | | | | |
| SOURCE | synthetic construct | | | | |
| ORGANISM | synthetic construct | | | | |
| | other sequences; artificial sequences. | | | | |

| | |
|--|--|
| ***** AUTHORS TITLE JOURNAL FEATURES source | Habben, J. E., Zinselmeier, C. and Tomes, D. Regulated expression of genes in plant seeds Patent: WO 0063401-A 8 26-OCT-2000; PIONEER HI-BRED INTERNATIONAL, INC. (US) Location/Qualifiers 1. .2722 |
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/note="Promoter from Hordeum vulgare, Plant Journal 6:849-860 (1994); gene from Agrobacterium tumefaciens, Molecular and General Genetics 216:388-394 (1988); terminator from Zea mays, Genbank Accession #S78780."

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ORIGIN

Alignment Scores:

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| Score: | 1230.00 | Matches: | 239 |
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| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| JB: | 2 | Gaps: | 0 |

US-10-817-483-2 (1-239) x AX039930 (1-2722)

QY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleLea 20
Db 1525 ATGGATCTTCAGCTAATTTTCGGTCCAACTGCGACAGGAAGAATCGATCGATAGCT 1584

QY 21 LeuAaIaGInIaThrGlyLeuProValIleuSerIleuAspArgValaGIncyScySProGIn 40
Db 1585 CTTCGCCAGACATGGCCCTCCCAAGTCTCTCGCTGCATCGCGTCCCAAGTGTCTCTCA 1644

QY 41 LeuSerThrClySerGlyArgProThrValGluGluLeuIysGlyThrThrArgLeuPyr 60
DB 1645 CTATCAACCGGAGCGGGGCACCAACAGCGAGCAATCAAAAGCAACGACTCGCTGTAC 1704

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| QY | 61 | LeuAaphaPaqPProLeuValVysGlyYlleLehrAlaVysGlnAlaHisGluAArgLeu | 80 |
| Db | 1705 | CTTATGATGTCCTCCCTTTGGTAAAGGGATCATTTACACCAAGCAAGCTCATGAACGGCTC | 1764 |
| QY | 81 | IlleaIagValHisAsnHisGluAlaVysGlyVglYleuLileuGlnGlyGlySerIle | 100 |
| Db | 1765 | ATTGGGGAGGTGCACATTCACGAGGCCAAAGCGGGCTTATTTCTTGAGGAGATCTATC | 1824 |
| QY | 101 | SerLeuLeuAArgCYsMetAlaGlnSerAArgYlrTriPasnAlaapPheAArgYlrHisIle | 120 |
| Db | 1825 | TCTGTTGCTCAGAGTCATAGCGCCAAAGTCATTATTTGAAACGGATTTTCGTGGCAATTT | 1884 |
| QY | 121 | IlleaArgAsnGluLeuAlaaspGluGluSerPheMetSerValAlaVsrHisValIys | 140 |
| Db | 1885 | ATTGCCAACGAGTTAGCAGACGAGAGAAAGCTTCATGAGCGTGCCCAAGACCAGAGTTAAAG | 1944 |
| QY | 141 | GlnMetLeuAArgProSerAlaGlyVleuSerIlelleGlnGluLeuValGlnLeuTriPArg | 160 |
| Db | 1945 | CAGATGTTACCCCTCTGCAGGCTTTCTTATTTCCAAAGAGTTGGTTCAACTTTGGAGG | 2004 |
| QY | 161 | GluProAArgLeuAArgProIleLeuGlnGlylleaspGlyYrAArgYrAlaLeuLeuPhe | 180 |
| Db | 2005 | GAGCTCGGCTGAGAGCCCATCTGAAAGGATTCATGATTCATATTCCTCTCTATTT | 2064 |
| QY | 181 | AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaaspMetGluAsn | 200 |
| Db | 2065 | GCTAACCCAGAACGATCATCGCCCGGATATGTTATTTGCAGCTCGACGCGAGATGGAGAT | 2124 |
| QY | 201 | LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaAArgAArgGlnGlnIlys | 220 |
| Db | 2125 | AAATTGATTACGGTATTCGCTCAGAGATTTCTTATTCATGCGCTCCACAGAAACAGAAA | 2184 |
| QY | 221 | PheProLeuValIleGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet | 239 |
| Db | 2185 | TTCCCTTTGGTGGGCGGACAGCTGTGAAACCGTTTAAAGACCAACCATTTCCGATG | 2241 |

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| | AUXO39931 | | | | | | | |
| | LOCUS | | 2722 bp | DNA | | linear | PAT 18-NOV-2000 | |
| | DEFINITION | AUXO39931 | Sequence 9 from Patent WO0063401. | | | | | |
| | ACCESSION | AUXO39931 | | | | | | |
| | VERSION | AUXO39931.1 | GI:11229960 | | | | | |
| | KEYWORDS | . | | | | | | |
| SOURCE | | synthetic construct | | | | | | |
| ORGANISM | | synthetic construct | | | | | | |
| REFERENCE | | other sequences; artificial sequences. | | | | | | |
| AUTHORS | 1 | Habben,J.E., Zinselmeyer,C. and Tomez,D. | | | | | | |
| TITLE | | Regulated expression of genes in plant seeds | | | | | | |
| JOURNAL | | Patent: WO 0063401-A 9 26-OCT-2000; | | | | | | |
| | | PIONEER HI-BRED INTERNATIONAL, INC. (US) | | | | | | |

FEATURES

Source

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/organism="synthetic construct"
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/db_xref="taxon:12630"
/note="Promoter from Zea mays, U.S. patent application
09/377,648; gene from Agrobacterium tumefaciens, Molecular
and General Genetics 216:388-394 (1989); terminator from
Solanum tuberosum, Plant Cell 1(1):115-122 (1989)."
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ORIGIN

Alignment Scores:

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| Score: | 1230.00 | Matches: | 239 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 2 | Gaps: | 0 |

US-10-817-483-2 (1-239) X AX039931 (1-2722)

QY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIaIeAla 20

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Db      1525  ATGATCTACGCTTAATTTTGGTCCAACTTCACAGAAAGACATCGACTCCGATAGCT 1584
Qy      21  LeuA1agiIntrnglyLeuProValleuSerLeuAparGValGInCysCysProGln 40
Db      1585  CTTGCCGACGACAGCTGGCTCCGAGTCTCTCGCTCGATCGCGTCCATATGCTGCTCAA 1644
Qy      41  LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyr 60
Db      1645  CTATCAACCGGAGCGGGCGACCAACAGTGAAGAACTGAAGAAAGCACTGCTGTGAC 1704
Qy      61  LeuAparAparProLeuValLysGlyLleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db      1705  CTTGATGATCGCCCTTTGGTAAAGGATATCATTAACGCCAAGCAAGCTCATGAAGCGCTC 1764
Qy      81  IleA1agiValHisAsnHisGluAlaLysGlyLysLleLeuGluGlyGlySerLle 100
Db      1765  ATTCGGAGGAGTGCAACATCACAGAGCCAAAGCGGGCTTATTTCTGAAGAGATCTATC 1824
Qy      101  SerLeuLeuArgCysMetAlaGlnSerArgTyrTriPheAlaAspPheArgTriHisLle 120
Db      1825  TCGTTGCTCAGAGTGATGCGCAAGTGTATTTGAACGCGGATTTTCGTTGGCATATT 1884
Qy      121  IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
Db      1885  ATTGGCAACGAGTTAGCAGACGAGAGAGCTTCATGACGCGCCAAACACAGACTTAAG 1944
Qy      141  GlnMetLeuArgProSerAlaGlyLeuSerLleIleGlnGluLeuValGlnLeuTriArg 160
Db      1945  CAGATGTTACGCCCTTGTGAGGTCTTCTATTATCAAGAGTTGTTCACTTTGGAGG 2004
Qy      161  GluProAlaGluLeuArgProLleLeuGluGlyLleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db      2005  GAGCTCGCGTGAAGGCCCATCTGAGAGGAGTGTGATGATTCGATGATGCCCTGTATT 2064
Qy      181  AlaThrGlnAsnGlnLleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
Db      2065  GCTACCCGAAACAGATACGCCCGCATATGCTATTGCGAGCTCGACGACGATATGAGAA 2124
Qy      201  LysLeuLleHisGlyLleAlaGlnGluPheLeuLleHisAlaArgArgGlnGluGlnLys 220
Db      2125  AAATTGATTACAGGATATCGCTCAGAGATTCTTAATCCATCGCGCGCAGAGAAACAGAA 2184
Qy      221  PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
Db      2185  TTCCCTTTGGTGGGCGCAGACTGTGCAAGCGTTTGAAGACCACTTTTCGAATG 2241

RESULT 5
AX039934      3017 bp      DNA      linear      PAT 18-NOV-2000
DEFINITION   Sequence 12 from Patent WO0063401.
ACCESSION    AX039934
VERSION      AX039934.1 GI:11229963
KEYWORDS
SOURCE
ORGANISM     synthetic construct
              other sequences; artificial sequences.
REFERENCE
1  Habben,J.E., Zinselmeier,C. and Tomes,D.
   TITLE      Regulated expression of genes in plant seeds
   JOURNAL    PIONEER HI-BRED INTERNATIONAL, INC. (US)
   LOCATION/Qualifiers
   SOURCE     1. .3017
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Promoter from Zea mays, Genbank Accession #U22344;
Gene from Agrobacterium tumefaciens, Molecular and General
Genetics 216:388-394 (1989); terminator from Zea mays,
Genbank Accession #L22345."

ORIGIN
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Pred. No.:      3 73e-126      Length:      3017
Score:          1230.00      Matches:      239
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    100.0%      Indels:      0
DB:             2      Gaps:      0

US-10-817-483-2 (1-239) x AX039934 (1-3017)

Qy      1  MetAspLeuArgLeuLlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
Db      1408  ATGATCTACGCTTAATTTTGGTCCAACTTCACAGAAAGACATCGACTCCGATAGCT 1467
Qy      21  LeuA1agiIntrnglyLeuProValleuSerLeuAparGValGInCysCysProGln 40
Db      1468  CTTGCCGACGACAGCTGGCTCCGAGTCTCTCGCTCGATCGCGTCCATATGCTGCTCAA 1527
Qy      41  LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyr 60
Db      1528  CTATCAACCGGAGCGGGCGACCAACAGTGAAGAACTGAAGAAAGCACTGCTGTGAC 1587
Qy      61  LeuAparAparProLeuValLysGlyLleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db      1588  CTTGATGATCGCCCTTTGGTAAAGGATATCATTAACGCCAAGCAAGCTCATGAAGCGCTC 1647
Qy      81  IleA1agiValHisAsnHisGluAlaLysGlyLysLleLeuGluGlyGlySerLle 100
Db      1648  ATTCGGAGGAGTGCAACATCACAGAGCCAAAGCGGGCTTATTTCTGAAGAGATCTATC 1707
Qy      101  SerLeuLeuArgCysMetAlaGlnSerArgTyrTriPheAlaAspPheArgTriHisLle 120
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Qy      121  IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
Db      1768  ATTGGCAACGAGTTAGCAGACGAGAGAGCTTCATGACGCGCCAAACACAGACTTAAG 1827
Qy      141  GlnMetLeuArgProSerAlaGlyLeuSerLleIleGlnGluLeuValGlnLeuTriArg 160
Db      1828  CAGATGTTACGCCCTTGTGAGGTCTTCTATTATCAAGAGTTGTTCACTTTGGAGG 1887
Qy      161  GluProAlaGluLeuArgProLleLeuGluGlyLleAspGlyTyrArgTyrAlaLeuLeuPhe 180
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Qy      181  AlaThrGlnAsnGlnLleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
Db      1948  GCTACCCGAAACAGATACGCCCGCATATGCTATTGCGAGCTCGACGACGATATGAGAA 2007
Qy      201  LysLeuLleHisGlyLleAlaGlnGluPheLeuLleHisAlaArgArgGlnGluGlnLys 220
Db      2008  AAATTGATTACAGGATATCGCTCAGAGATTCTTAATCCATGCGCGCAGAGAAACAGAA 2067
Qy      221  PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
Db      2068  TTCCCTTTGGTGGGCGCAGACTGTGCAAGCGTTTGAAGACCACTTTTCGAATG 2124

RESULT 6
AX039929      5622 bp      DNA      linear      PAT 18-NOV-2000
DEFINITION   Sequence 7 from Patent WO0063401.
ACCESSION    AX039929
VERSION      AX039929.1 GI:11229958
KEYWORDS
SOURCE
ORGANISM     synthetic construct
              other sequences; artificial sequences.
REFERENCE
1  Habben,J.E., Zinselmeier,C. and Tomes,D.
   TITLE      Regulated expression of genes in plant seeds
   JOURNAL    PIONEER HI-BRED INTERNATIONAL, INC. (US)
   LOCATION/Qualifiers
   SOURCE     1. .3017
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
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              /note="Promoter from Zea mays, Genbank Accession #U22344;
Gene from Agrobacterium tumefaciens, Molecular and General
Genetics 216:388-394 (1989); terminator from Zea mays,
Genbank Accession #L22345."

ORIGIN
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FEATURES
source
Location/Qualifiers
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/note="Promoter and terminator from Zea mays as found in Genbank. Accession #S78780; gene from Agrobacterium tumefaciens as found in Molecular and General Genetics 216:388-394 (1989)."

ORIGIN

Alignment Scores:
Pred. No.: 8,99e-126 Length: 5622
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-817-483-2 (1-239) x AK039929 (1-5622)

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DB 1525 ATGATCTACGCTCAATTTTCGGTCCCACTTGCAAGAAACATCGATCGATAGCT 1584
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 1585 CTTGCCACAGACAGCTGCTCCAGTCTCTCGCTCGATCGGTCCAATGCTGCTCTCA 1644
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuGlyGlyThrThrArgLeuTyr 60
DB 1645 CTATCAACCGGAAGCGGCGACCAACAGTGAAGAACTGAAGAAACGACTGCTGATC 1704
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB 1705 CTTGATGATCGCCCTTTGGTAAAGGATCATTTACAGCCAAAGCTCATAGACGGCTC 1764
QY 81 IleAlaGluValHisAsnHisGluAlaLysGlyLeuIleLeuGluGlyLysSerIle 100
DB 1765 ATTCGAGAGTGCACATCATCAGAGCCAAAGCGGCTTATTTCTGAGGAGGATCTATC 1824
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 1825 TCGTTGCTCAGGTGATGCGCAAGTCTTATTTGAAACGCGATTTTCGTTGCAATAT 1884
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
DB 1885 ATTCGACACGAGTTGACAGACGAGAGACCTCATAGCGTGGCCAAAGCCAGAGTTAAG 1944
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 1945 CAGATGTTACGCCCTCTGCAAGTCTTTCTATTATTCAAAGATGGTTCACATTTGGAGG 2004
QY 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 2005 GAGCCTCGGCTGAGGCCCATCTAGAAAGGATCGATGATATCATGCTCCCTGCTATTT 2064
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 2065 GCTACCCAGAACCAAGATCCGCCCATATGCTATTGACAGCTCGACCGACAGATTTGAGAA 2124
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnLys 220
DB 2125 AAATTGATTCACGATATCGCTCAGGAGTTTCTAATCATGCGCGTCGACAGGAACAGAA 2184
QY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
DB 2185 TTCCCTTTGGTGGGCGCACAGCTGTGAAAGCGTTGAAGACCACTATTTGAAATG 2241

RESULT 7
CQ899250 723 bp DNA linear PAT 08-NOV-2004
LOCUS CQ899250
DEFINITION Sequence 2 from Patent WO2004092390.

ACCESSION CQ899250
VERSION CQ899250.1 GI:55583090
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Monsanto Technology LLC (US)
Patent: WO 2004092390-A 2 28-OCT-2004;
Dna constructs and methods to enhance the production of commercially viable transgenic plants
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.

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Location/Qualifiers
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Alignment Scores:
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Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 2 Gaps: 0

US-10-817-483-2 (1-239) x CQ899250 (1-723)

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QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTTGCCACAGACAGCTGCGCTTTCAGTCTTTCGCTCGATCGGTCCAATGTTGCTCTAG 120
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB 121 CTTGATGATCGCCCTCTGTAAGGATTCATCGACGCAAGCAAGCTCATGAAAGGCTG 180
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB 181 CTTGATGATCGCCCTCTGTAAGGATTCATCGACGCAAGCAAGCTCATGAAAGGCTG 240
QY 81 IleAlaGluValHisAsnHisGluAlaLysGlyLeuIleLeuGluGlyLysSerIle 100
DB 241 ATGGGGAGGTGTATATATATATGAGGCCACGCGGCGCTTATTTCTGAGGAGGATCTATC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 301 TCGTTGCTCAGTGTATGATGCGCAAGCATTTATGAGATGCGGATTTTCGTTGGCATAT 360
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
DB 361 ATTCGACACGAGTTGACAGACGAGACGCTTCAAGAACGTGGCCAAAGCCAGAGTTAAG 420
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACGCCCTCTGCAAGTCTTTCTATTATTCAAAGATGGTTCATTTGGAA 480
QY 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 481 GAGCCTCGGCTGAGGCCCATCTGAAAGATCGATGATATCATGATATGCTATGTTGTT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 541 GCTACCCAGAACCAAGATCCCATATGCTATTGACAGCTTGAACGCAATATGAGAGAT 600
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnLys 220
DB 601 AAGTTGATTCATGAGATGCTCAGAGATATCTCATTCATGACGCCGACAGAACAGAA 660

OY 221 PheProLeuVal1G1yAla1ThrAla1Val1Glu1Ala1PheGlu1Gly1ProProPheArgMet 239
DB 661 TTCCTCGAGTTAAGCGACGCCGCTTAAGAGATTCAGAGTTCATTCATTCGGAATG 717

RESULT 8
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DEFINITION Agrobacterium tumefaciens pTiT37 T-DNA tmr locus.
ACCESSION X00639.1 GI:944822
VERSION X00639.1
KEYWORDS cycokinin; plasmid.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens (Rhizobium radiobacter); Rhizobiales; Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.

REFERENCE
1 (bases 1 to 1982)
AUTHORS Goldberg, S.B., Flick, J.S. and Rogers, S.G.
TITLE Nucleotide sequence of the tmr locus of Agrobacterium tumefaciens pTi T37 T-DNA
JOURNAL Nucleic Acids Res. 12 (11), 4665-4677 (1984)
PUBMED 6330678
COMMENT On Aug 15, 1995 this sequence version replaced gi:39174.
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Alignment Scores:
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Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
Gaps: 0

US-10-817-483-2 (1-239) x ATTMRPT (1-1983)

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OY 21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysGlyProGln 40
DB 719 CTGGCCAGCAGACGCGCTTCACATCTTCGCTCGATCGGCTCAATGTGTCTCAG 778

OY 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyr 60
DB 779 CTGTCAACCGGAAGCGACGACCAAGTGGAGAACTGAAAGCAAGACCGCTTATAC 838

OY 61 LeuAspAspArgProLeuValIleGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB 839 CTTGATGATCGGCTCTGCTGTAAGGGTATCATTCGACCAAGCAAGCTCATGAAAGGCTG 898

OY 81 IleAlaGluValHisAsnHisGluAlaIleGlyGlyLeuIleLeuGluGlySerIle 100
DB 899 ATGGGAGAGGTATTAATTTATAGAGCCACGCGCGCTTATCTTGAGGGAGATCTATC 958

OY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 959 TCGTTGCTCAAGTGCATCGCGCAAGCAGTATTTGAGTGGCATTTTCGTTGGCATATT 1018

OY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValIys 140
DB 1019 ATTCGCCACGAGTTAGACGACGAAAGACCTTCATGAACTGGCCAGGCGCAGGTAAAG 1078

OY 141 GluMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 1079 CAGAGTTAGCCCTCGCTGAGGCGCTTCTATTTTCCAGAGTTGGTTGATCTTGGAAA 1138

OY 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuPhe 180
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OY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
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OY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnIys 220
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OY 221 PheProLeuVal1G1yAla1ThrAla1Val1Glu1Ala1PheGlu1Gly1ProProPheArgMet 239
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RESULT 9
AE007927 9931 bp DNA linear BCT 28-MAY-2004
LOCUS Agrobacterium tumefaciens str. C58 plasmid T1, section 5 of 20 of the complete sequence.
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ACCESSION AE007927 AE007871
VERSION AE007927.2 GI:16271969
KEYWORDS
SOURCE
ORGANISM
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Agrobacterium tumefaciens str. C58
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.

REFERENCE
1 (bases 1 to 9931)
Hinkle, G., Slater, S.C. and Goodner, B.
TITLE Complete Genome Sequence of Agrobacterium tumefaciens C58 (Rhizobium radiobacter C58), the Causative Agent of Crown Gall Disease in Plants
JOURNAL Unpublished
AUTHORS Hinkle, G., Slater, S.C. and Goodner, B.
REFERENCE 2 (bases 1 to 9931)
Hinkle, G., Slater, S.C. and Goodner, B.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street, Cambridge, MA 02139, USA
COMMENT On Oct 19, 2001 this sequence version replaced gi:15163470.
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ORIGIN
Alignment Scores:
Pred. No.: 3,71e-108 Length: 9931
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 15 Gaps: 0
US-10-817-483-2 (1-239) x AB007927 (1-9931)
QY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLeuThrSerThrAlaIleAla 20
Db 6116 ATGATCTCGCGCTAATTTTCGCTCCAACTTGCACAGAAACGTCGACCGCGGAGCT 6175
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 6176 CTTGGCCGACGACGCGGCTTCCAACTCTTTCGCTCGATCGGGTCCAAATGTGCTCTCAG 6235
QY 41 LeuSerThrGlySerGlyAlaArgProThrValGlnGluLeuLeuGlyLeuThrThrArgLeuYr 60
Db 6236 CTGTCAACCGGAGGAGGACGACCAACAGTGAAGAACGTGAAGAACGAGCCGCTTATAC 6295
QY 61 LeuAspAspArgProLeuValLeuGlyIleIleThrAlaLeuGlnAlaHisGlnArgLeu 80
Db 6296 CTTGATGATCGGCTCTGCTGGAAGGATCATCGACGCAACCAAGCTCATGAAGGCTG 6355
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Db 6416 TCGTTGCTCAAGTGTGATGGCGAAAGCAGTTATTGAGAGCGGATTTTCGTTGGCATATT 6475
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLeuThrArgValLeu 140
Db 6476 ATTCGCCACGAGTTAGCAGACGAGACGACCTTCAAGACGTCGCAAGGCCACGAGTTAAG 6535
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Db 6536 CAGATGTTAAGCCCTGCGTGCAGAGGCTTTCTATTATTCAAAGAGTTGGTGCATCTTGA 6595
QY 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyYrYrArgTrpAlaLeuLeuPhe 180
Db 6596 GAGCTCTGCGTGGAGCCCATATGAAAGAGATCGATGATATCGATATGCGATGTGTTT 6655
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 6656 GGTACGCAAGAACCAATCACAATCCGATATGCTATTCGACGCTTGAACGAGATATGAGGAT 6715
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgAlaGlnGluGlnLys 220

| | | | |
|------------|--|--|--------|
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| Oy | 221 | PheProLeuVal1G1yAlaThrAlaVal1G1ua1aPheGluGlyProProPheArgMet | 239 |
| Db | 6776 | TTCCCTCGAGTTAACGACGACCGCTTACGACGATTCGAAAGTTCATCCATTCGGAATG | 6832 |
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| DEFINITION | 10377 bp | DNA | linear |
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| SOURCE | | | |
| ORGANISM | Agrobacterium tumefaciens str. C58 | | |
| REFERENCE | | | |
| AUTHORS | Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Woo, L., Kitajima, J.P., Okura, V.K., Almeida, N.F., Jr., Zhou, Y., Boye, D. Sr., Chapman, P., Clendenning, J., Deatherage, G., Gillet, M., Grant, C., Guenther, D., Kutyavin, T., Levy, R., Li, M., McCelland, E., Palmieri, A., Raymond, C., Rouse, G., Saenphimachak, C., Wu, Z., Gordon, D., Eisen, J.A., Paulsen, I., Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M., Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V., and Nester, E.W. | | |
| TITLE | The genome of the natural genetic engineer Agrobacterium tumefaciens C58 | | |
| JOURNAL | Science | 294 (5550), 2317-2323 | (2001) |
| REFERENCE | 11743193 | | |
| AUTHORS | 2 (bases 1 to 10377) | | |
| | Wood, D.W., Setubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E., Chen, Y., Woo, L., Kitajima, J.P., Okura, V.K., Almeida, N.F., Jr., Zhou, Y., Boye, D. Sr., Chapman, P., Clendenning, J., Deatherage, G., Gillet, M., Grant, C., Guenther, D., Kutyavin, T., Levy, R., Li, M., McCelland, E., Palmieri, A., Raymond, C., Rouse, G., Saenphimachak, C., Wu, Z., Gordon, D., Eisen, J.A., Paulsen, I., Karp, P., Romero, P., Zhang, S., Yoo, H., Tao, Y., Biddle, P., Jung, M., Zhao, Z., Dolan, M., Tingey, S.V., Tomb, J., Gordon, M.P., Olson, M.V., and Nester, E.W. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (27-SEP-2001) | Department of Microbiology, University of Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA | |
| FEATURES | 98195..7242, USA | | |
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ORIGIN

Alignment Scores:
Pred. No.: 3,95e-108 Length: 10377
Score: 1075..00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 15 Gaps: 0

US-10-817-483-2 (1-239) x AE009419 (1-10377)

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Db 9428 CTGGCCAGCAGACTGGGCTTCCAACTCTTCGCTCGATCCGGGTCCAAATGTTGTCTCAG 9487
QY 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyIleThrThrArgLeuTyr 60
Db 9488 CTGTCACACCGAAGCGAGCAGCAACAAGTGGAGAACTGAAAGAACACAGCGCTTATAC 9547
QY 61 LeuAapAapArgProLeuValIleGlyIleIleThrAlaLysGlnAlaHisGluAaArgLeu 80
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QY 81 IleAlaGluValHisAsnHisGluValLysGlyGlyLeuIleLeuGluGlyGlySerIle 100

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| Oy | 181 | AlaThrGlnAngGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn | 200 |
| Db | 9908 | GCTTACCGCAAGAACCGATCCGATCCGATATGCAAGCTTGACGTCAGAGATATGAGAGAT | 9967 |
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| Oy | 221 | PheProLeuValGlyAlaThrAlaValGlnAlaPheGluGlyProProPheArgMet | 239 |
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| ACCESSION | AB016260 | AB006857 | AB006858 |
| VERSION | AB016260.1 | GI:6498173 | |
| KEYWORDS | Agrobacterium tumefaciens (Rhizobium radiobacter) | | |
| SOURCE | Agrobacterium tumefaciens (Rhizobium radiobacter) | | |
| ORGANISM | Rhizobiales; Rhizobiaceae; Agrobacterium. | | |
| REFERENCE | 1 Hattori,Y., Suzuki,K., Uraji,M., Ohta,N., Katoh,A. and Yoshida,K. | | |
| AUTHORS | Genome structure of pTi-SAKURA (I): strategy for DNA sequencing of | | |
| TITLE | Nucleic Acids Symp. Ser. 37, 159-160 (1997) | | |
| JOURNAL | 9586048 | | |
| PUBMED | 2 | | |
| REFERENCE | Hattori,Y., Suzuki,K., Ohta,N., Uraji,M., Katoh,A. and Yoshida,K. | | |
| AUTHORS | Genome structure of pTi-SAKURA (V): Complete nucleotide sequence of | | |
| TITLE | plasmid pTi-SAKURA's vir region in Agrobacterium tumefaciens | | |
| JOURNAL | Nucleic Acids Symp. Ser. 39, 265-266 (1998) | | |
| PUBMED | 3 | | |
| REFERENCE | Ohta,N., Suzuki,K., Hattori,Y., Uraji,M., Katoh,A. and Yoshida,K. | | |
| AUTHORS | Genome structure of pTi-SAKURA (III): Characteristics of T-DNA | | |
| TITLE | Nucleic Acids Symp. Ser. 39, 185-186 (1998) | | |
| JOURNAL | 4 | | |
| PUBMED | Uraji,M., Suzuki,K., Ohta,N., Hattori,Y., Katoh,A. and Yoshida,K. | | |
| REFERENCE | Genome structure of pTi-SAKURA (IV): Characteristics of tra region | | |
| AUTHORS | Nucleic Acids Symp. Ser. 39, 187-188 (1998) | | |
| TITLE | 5 | | |
| JOURNAL | Suzuki,K., Ohta,N., Hattori,Y., Uraji,M., Kato,A. and Yoshida,K. | | |
| PUBMED | Novel structural difference between nopaline- and octopine-type | | |
| REFERENCE | trbD genes: construction of genetic and physical map and sequencing | | |
| AUTHORS | of trbD/trai and rep gene clusters of a new Ti plasmid pTi-SAKURA | | |
| TITLE | Biochem. Biophys. Acta 1396 (1), 1-7 (1998) | | |
| JOURNAL | 6 | | |
| PUBMED | Suzuki,K., Hattori,Y., Uraji,M., Ohta,N., Iwata,K., Murata,K., | | |
| REFERENCE | Kato,A. and Yoshida,K. | | |
| AUTHORS | Complete nucleotide sequence of a plant tumor-inducing Ti plasmid | | |
| TITLE | Gene 242 (1-2), 331-336 (2000) | | |
| JOURNAL | | | |

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PUBLISHED 10721727
REFERENCE 7 (bases 1 to 206479)
AUTHORS Suzuki, K. and Yoshida, K.
TITLE Direct Submission
JOURNAL Submitted (22-JUL-1998) Kazuo Yoshida, Hiroshima University,
Faculty of Science, Kagamiyama 1-3-1, Higashihiroshima-shi,
Hiroshima 735, Japan (E-mail:ksuzuki@ipc.hiroshima-u.ac.jp,
Tel:0824-24-7456, Fax:0824-24-0733)
On or before May 14, 2001 this sequence version replaced
gi:2982699, gi:2982703.
COMMENT Location/Qualifiers
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Alignment Scores:
Pred. No.: 1.74e-106 Length: 29524
Score: 1066.00 Matches: 205
Percent Similarity: 93.3% Conservative: 18
Best Local Similarity: 85.8% Mismatches: 16
Query Match: 86.7% Indels: 0
DB: 15 Gaps: 0

US-10-817-483-2 (1-239) x ATU237588 (1-29524)

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QY 21 LeuAlaGInGInThrGlyLeuProValLeuSerLeuAspArgValGInCysCysProGln 40

Db 23015 CTTGCCACAGACTGGCTTCCAGTCTTTCCTGCTGATCGGCTCCAAATGTTCTCTCAG 23074
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Db 23075 CTGTCAACCGGAAGCGGACGACCAACAGTGGAAAGAACTGAAAGAAAGAGCCGCTATATC 23134
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Db 23135 CTTGAATGATCGGCTCTGTGTGAAGGGTATCATTCGCAAGCAAGCACTCATGAAAGCTG 23194
QY 81 IleAlaGluValHisAsnHisGluAlaLysGlyGlyLeuIleLeuGluGlyGlySerIle 100
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Db 23375 CAGATGTTACGCCCTCTCTCAGAGCCCTTTCTATTTATCCAAAGATTGGTTGATCTTGGAAA 23434
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QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnLys 220
Db 23555 AAGTTGATTCATCGGATCTCTCAGAGATCTTCATTCATCATGACGCGGACAGAGAGAAA 23614
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Db 23615 TTCCCTCGAGTTAAGCGACCGCTTACAGCGGATTCGAAAGTCAATTCGGAATG 23671
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AB025109 1997 bp DNA linear BCT 27-MAR-1999
LOCUS AB025109
DEFINITION Agrobacterium tumefaciens gene for isopentenyl transferase,
complete cds.
ACCESSION AB025109
VERSION AB025109.1 GI:4586309
KEYWORDS isopentenyl transferase.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE 1 (bases 1 to 1997)
AUTHORS Kasahara,T., Sugita,K., Ebinuma,H., Endo,S., Kawaoka,A. and
Moriwae,N.
TITLE Agrobacterium tumefaciens plasmid P022 isopentenyl transferase (ipt)
gene
JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 1997)
AUTHORS Kasahara,T., Sugita,K., Ebinuma,H., Endo,S., Kawaoka,A. and
Moriwae,N.
TITLE Direct Submision
JOURNAL Submitted (18-MAR-1999) Takehide Kasahara, Nippon Paper Industries
Co Ltd, R&D Div., Wood Bio-engineering Central Research Lab.,
5-21-1, Oji, Kita-ku, Tokyo 114-0002, Japan
(E-mail:takehemcj.biglobe.ne.jp, Tel:81-3-3911-5106 (ex.292),
Fax:81-3-3914-3350)
FEATURES
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ORIGIN
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Query Match: 85.5% Indels: 0
DB: 15 Gaps: 0
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QY 21 LeuAlaGlnGlnInThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 748 CTTGCCACAGACATCGGCGCTTCCAGTCTTTCGCTGCGAGCGGGTCCAAATGTTGCTCTCAG 807
QY 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyr 60
Db 808 CTGTCAACCGGAAGCGAGACCAACAGTGAAGAAGTGAAGAAACAGACCGCTCTATAC 867
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db 868 CTTGATGATCGGCTCTGCTGTAAGGATATCATCGCAAGCAACAGCTCATGAAAGGCTG 927
QY 81 IleAlaGluValHisAsnHisGluAlaLysGlyGlyLeuIleLeuGluGlyGlySerIle 100
Db 928 ATGGGAGAGGTGTAATTAATTAAGGCCACGCGCGGCTTATTTCTGAAGAGAGATCTATC 987
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTyrAsnAlaAspPheArgTrpHisIle 120
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Db 1108 CAGATGTTAAGCGCCGCTTCAAGCTTCTATTAACAAGATGTTGATCTTGGAAA 1167
QY 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
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QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 1228 GTTACCCAGAACCAATCATCCATATGCTATGCTGAGCTTGACGAGATATGAGAGAT 1287
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnLys 220
Db 1288 AAGTTGATTCATGGATGCTCAGAGATATCTCATTCATGCAAGCCGCAAGAAACAGAAA 1347
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RESULT 14
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DEFINITION Plasmid T1 (from A. tumefaciens Tm-4) ipt gene for cytokinin.
ACCESSION  X17428
VERSION    X17428.1 GI:45558
KEYWORDS   cytokinin; ipt gene; T1 plasmid.
SOURCE     Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
            Rhizobiaceae; Agrobacterium.
REFERENCE  1 (bases 1 to 1382)
            Bonnard,G., Tinland,B., Paulus,F., Szegedi,E. and Otten,L.
            Nucleotide sequence, evolutionary origin and biological role of a
            rearranged cytokinin gene isolated from a wide host range biotype
            III Agrobacterium strain
            Mol. Gen. Genet. 216 (2-3), 428-438 (1989)
JOURNAL    PUBMED
FEATURES   location/Qualifiers
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            Best Local Similarity: 85.2%      Mismatches:  19
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            QY      21 LeuAagIngtInThrglyLeuProValLeuSerLeuAaPArgValGlnCysCysProGln 40
            Db      272 CTTCCGCCGACAGACTGGGCTTCACATCTTCCTCGCTCGATCGGCTCCAAATGCTGCTCAG 331
            QY      41 LeuSerThrglySerGlyAArgProThrValGlnGluGluLeuLysGlyThrThraGlyLeuTyr 60
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            QY      61 LeuAspAaPArgProLeuValLysGlyIleIleThraIalyGlnAlaIleGluAArgLeu 80
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QY      81 IleAagIValaHisAenHisGluAlaLysGlyLeuIleLeuGlnGlySerIle 100
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QY      101 SerLeuAaArgCysMetAlaGlnSerAArgTyrTrpAsnAlaAspPheArgTyrHisIle 120
Db      512 TCGTTGCTCAAGTCAATGCGCCCAAGCGGTTATGAGACCGCGATTTTCGTGCAATAT 571
QY      121 IleArgAsnGluLeuAlaAspGlnGluSerPheMetSerValAlalystrAryVallys 140
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QY      181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAaPAlaAspMetGluAsn 200
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QY      221 PheProLeuValGlyAlaThraValaGluAaPheGlnGlyProProPhe 237
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RESULT 15
ATTALAAH
LOCUS      10200 bp      DNA             linear      BCT 18-APR-2005
DEFINITION A. tumefaciens Tm4 T1 plasmid DNA with TA-iaaH interrupted by 18866,
            TA-iaaM, T-1pt and T-6 genes.
ACCESSION  X56185
VERSION    X56185.1 GI:39133
KEYWORDS   iaaH gene; iaaM gene; indoleacetamide hydrolase; ipt gene;
            isopentenyl transferase; cryptophane monooxygenase.
SOURCE     Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
            Rhizobiaceae; Agrobacterium.
REFERENCE  1 (bases 7402 to 8783)
            Bonnard,G., Tinland,B., Paulus,F., Szegedi,E. and Otten,L.
            Nucleotide sequence, evolutionary origin and biological role of a
            rearranged cytokinin gene isolated from a wide host range biotype
            III Agrobacterium strain
            Mol. Gen. Genet. 216 (2-3), 428-438 (1989)
JOURNAL    PUBMED
FEATURES   location/Qualifiers
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ORIGIN
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Pred. No.: 2,35e-105 Length: 10200
Score: 1050.00 Matches: 202
Percent Similarity: 92.04 Conservative: 16
Best Local Similarity: 85.24 Mismatches: 19
Query Match: 85.44 Indels: 0
DB: 15 Gaps: 0
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QY 1 MetAapLeuAaYgLeuIlePheGlyProThrCySthrgYlySthSerThraIleAa 20
Db 7613 ATGATTCGCGCTTAAATTTTCGCTCAACTGCACAGAAAGACGTCAACGCGATAGCT 7672
QY 21 LeuAaGInGIntHrgYleuProValLeuSerLeuAaPaYVaIGInCySYPProGIn 40
Db 7673 CTGCGCCAGCAGACGTGGCTTCAGTCTTTTCGCTCGATCGGCTCAATGCTGCTCAG 7732
QY 41 LeuSerThrgYleSergYlaYgProThraValGInGInleuAaYgYThThraYgLeuYr 60
Db 7733 CTGTCACACCGAAGCGGACGACCAACAGTGAAGAACTGAAGAAACACCCGCTGTAC 7792
QY 61 LeuAaPaPaYgProLeuValYleGlyIleIleThraIaYsGInAaHieGInYgLeu 80
Db 7793 CTTGATGATCGGCCCCCTGTGAAGGGATCATCGACGCCGACCAAGCTCATAGAGGCTG 7852
QY 81 IleAaGInVaIHaSnhIeGInAaYsGInYleuIleleuGInGlyYgYserIle 100
Db 7853 ATCCGCGAGGTGTATTAATTAGAGGCCACCGCGCATTAATTCTGAGAGGAGTACTAT 7912
QY 101 SerLeuLeuAaYgCyMeAaIeGInSeraYgYrTTPaanaIaPaPheAaYgTrpHisIle 120
Db 7913 TCGTTGCTCAAGTGCATGCGCCAAAGCCGTTATTGAGCGCCGATTTTCGTTGCAATAT 7972
QY 121 IleAaGInGInleuAaIaPaGInGInleuSerPheMeSerValAaIaYThraYgValys 140
Db 7973 ATTCGCCACAAAGTTAGACGAGGAGACCTTCATGAAGCGCCAGACCTTAAAG 8032
QY 141 GInMeIleAaYgProSeraIeGlyLeuSerIleIeGInGInleuValGInleuYrPaYg 160
Db 8033 CAGATGTTGTCGCCCGCATAGGCCCATCTCTATTCAAGAGTTGTTATCTTTGCAAT 8092
QY 161 GluProAaYgLeuAaYgProIleleuGInGlyIleAaPgiYrYrAaYgYrAaIeAaPhe 180
Db 8093 GAGCTCGCGTGAAGGCCCATATCTGAAGAGATCATGATATCATGATATGATGTTGTTT 8152
QY 181 AlaThrgInaGInIleThrProAaPMeIleuGInleuAaPaIaAaPMeGInAa 200
Db 8153 GCTAGCCAGAAATCGGATACCCCGCATATGCTATTGAGCTTGAGCGAGATATGAGAGGT 8212
QY 201 LysLeuIleHieGlyIleAaGInGInPheLeuIleHieSaIaAaYgGInGInGInYs 220
Db 8213 AAGTTGATTCATGGATGCTCAGAGAGATCTCATTCATGCGCGTCCAGAACACAGAA 8272
QY 221 PheProLeuValGlyAaIaThraIaValGInAaPheGInGInYrProProPhe 237
Db 8273 TTCCGCGCGGTGAGGCGGCGGAGCTTTGAAAGATTGAAGGCCACCACTTC 8323
Search completed: June 26, 2006, 21:30:23
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Job time : 5814 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: June 26, 2006, 19:29:08 ; Search time 652 Seconds
(without alignments)
3833.667 Million cell updates/sec

Title: US-10-817-483-2

Perfect score: 1230
Sequence: 1 MDLRLIFGPTCTGKTSTAIA.....KPLVGAATVAEAFEGPPFRM 239

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/abs/ABSWEB_spool/US10817483/runatc_26062006_142740_18750/app_query.fasta_1
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-MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|---------------------|
| 1 | 1230 | 100.0 | 717 | 13 | AD863261 Bacterial |
| 2 | 1230 | 100.0 | 721 | 3 | AAc86514 Nucleotide |
| 3 | 1230 | 100.0 | 723 | 10 | ACF58155 Z. mays 1 |

| | | | | | |
|----|------|-------|-------|----|--------------------|
| 4 | 1230 | 100.0 | 1919 | 13 | ADT92127 A. tumef |
| 5 | 1230 | 100.0 | 2722 | 3 | AAc86508 DNA const |
| 6 | 1230 | 100.0 | 2722 | 3 | AAc86507 DNA const |
| 7 | 1230 | 100.0 | 3017 | 3 | AAc86511 DNA const |
| 8 | 1230 | 100.0 | 5622 | 3 | AAc86506 DNA const |
| 9 | 1075 | 87.4 | 720 | 13 | AD863280 Bacterial |
| 10 | 1075 | 87.4 | 720 | 13 | AD863264 Bacterial |
| 11 | 1075 | 87.4 | 720 | 13 | AD859368 Bacterial |
| 12 | 1075 | 87.4 | 720 | 13 | AD862875 Bacterial |
| 13 | 1075 | 87.4 | 723 | 13 | ADT62691 DNA encod |
| 14 | 1068 | 86.8 | 723 | 13 | ADRA42934 IPT-like |
| 15 | 1068 | 86.8 | 723 | 13 | ADRA42936 IPT-like |
| 16 | 1068 | 86.8 | 723 | 15 | AEFI4553 Isopen |
| 17 | 1068 | 86.8 | 723 | 15 | AEFI4572 Isopen |
| 18 | 1066 | 86.7 | 720 | 13 | AD863295 Bacterial |
| 19 | 1052 | 85.5 | 720 | 13 | AD863294 Bacterial |
| 20 | 1052 | 85.5 | 1997 | 12 | AD855756 Agrobacte |
| 21 | 1050 | 85.4 | 720 | 13 | AD863275 Bacterial |
| 22 | 1050 | 85.4 | 720 | 13 | AD863279 Bacterial |
| 23 | 1050 | 85.4 | 723 | 13 | ADRA42938 IPT-like |
| 24 | 1050 | 85.4 | 723 | 15 | AEFI45470 Isopen |
| 25 | 1050 | 85.4 | 723 | 15 | AEFI45468 Isopen |
| 26 | 1050 | 85.4 | 723 | 15 | AAV69757 Isopen |
| 27 | 1035 | 84.1 | 777 | 13 | AD863297 Bacterial |
| 28 | 1005 | 81.7 | 720 | 13 | AD863266 Bacterial |
| 29 | 1005 | 81.7 | 720 | 13 | AD863290 Bacterial |
| 30 | 1005 | 81.7 | 720 | 13 | AD863262 Bacterial |
| 31 | 1005 | 81.7 | 720 | 13 | AD863292 Bacterial |
| 32 | 1005 | 81.7 | 723 | 3 | AAV00619 Agrobacte |
| 33 | 1005 | 81.7 | 745 | 2 | AAV69757 Isopen |
| 34 | 1005 | 81.7 | 1988 | 6 | ABK12492 Agrobacte |
| 35 | 1005 | 81.7 | 2595 | 11 | ADJ99856 IPT gene |
| 36 | 1005 | 81.7 | 2595 | 11 | ADL73033 Agrobacte |
| 37 | 1005 | 81.7 | 2595 | 14 | ADX98862 Isopen |
| 38 | 1005 | 81.7 | 9323 | 10 | ADJ99857 Binary ve |
| 39 | 1005 | 81.7 | 9323 | 14 | ADX98863 Plasmid p |
| 40 | 1005 | 81.7 | 24596 | 1 | AAV50182 Complete |
| 41 | 995 | 80.9 | 3182 | 6 | AAV33336 A. thalia |
| 42 | 995 | 80.9 | 24593 | 1 | AAV50226 Sequence |
| 43 | 994 | 80.8 | 747 | 3 | AAV00624 Agrobacte |
| 44 | 994 | 80.8 | 3183 | 6 | AAV33601 A. thalia |
| 45 | 984 | 80.0 | 3183 | 2 | AAV42919 SAG12-1 p |

ALIGNMENTS

RESULT 1
AD863261
ID AD863261 standard; cDNA; 717 BP.
XX
AC AD863261;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #15248.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.

XX (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 38935; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 717 BP; 180 A; 176 C; 190 G; 171 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1,16e-132 Length: 717
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0
US-10-817-483-2 (1-239) x ADS63261 (1-717)
QY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 1 ATGATCTACGCTTAATTTTGGTCCAACTTGCAAGAGAAAGACATCAGCTCGCATTA 60
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTTCGCCAGCAGACTGGCTCCCACTCTCGCTCGATCCGATCCCAATGCTGCTCTCA 120
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuLys 60
DB 121 CTATCAACCGGAAGGGGCGAACCAAGTGAAGAACTGAAGGAACCACTCGCTGTGAC 180
QY 61 LeuAspArgProLeuValLeuGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu 80
DB 181 CTGATGATCGCCCTTTGGTAAAGGTATCATTAACGCAAGCAAGCTCATGAACGGCTC 240
QY 81 IleAlaGluValHisAsnHisGlnAlaLysGlyLeuIleLeuGluGlyGlySerIle 100
DB 241 ATTGGGAGGTGACCAATCAACAGGCGCAAGGGCGGCTTATCTTGAAGGAGATCTATC 300

QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 301 TCGTTGCTCAGTGCATGAGCGCAAGTGTATTGAAACGGGAAATTTTCGTTGGCATATT 360
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
DB 361 ATTGCACAAGAGTTAGCAGACAGAGAGAGCTTATGAGCGTGGCCAGACCAAGATTAA 420
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACCGCCCTCTGCAAGTCTTCTATTATTCAGAGGTGGTTCACTTGGAGG 480
QY 161 GluProArgLeuAspProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 481 GAGCCTCGGCTGAGGCCCATCTGAAAGGATCATGATTCATATGCTCCCTCTATT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 541 GCTACCCAGAAACAGATCAGCCCGATATGCTATTGACAGCTCGACGAGATATGAGAA 600
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
DB 601 AAATTGATTCAAGGTATCGCTCAGAGATTCTTAATTCATGCGCGCTCGACAGAA 660
QY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
DB 661 TTCCTTTGGTGGCGGACAGCTGTGAAAGCATTGAAGCACCATTTTCGAATG 717
RESULT 2
AAC86514
ID AAC86514 standard; DNA; 721 BP.
XX
AC AAC86514;
XX
DT 19-MAR-2001 (first entry)
XX
DE Nucleotide sequence of an isopenentenyl transferase (lpt) gene fragment.
XX
KM temporal gene expression; spatial gene expression; plant seed;
KM cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KM yield stability; tip kernel abortion; seed set; isopenentenyl transferase;
KM lpt; ss.
XX
OS Agrobacterium tumefaciens.
XX
PN WO20063401-A1.
XX
PD 26-OCT-2000.
XX
PE 13-APR-2000; 2000WO-US009943.
XX
PR 16-APR-1999; 99US-0129844P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Habben JE, Zinselmeier C, Tomes D;
XX
DR WPI; 2000-672743/65.
XX
PT Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.
XX
PS Disclosure; Page 16; 76pp; English.
XX
CC The present sequence represents an isopenentenyl transferase gene fragment.
CC The fragment was used to produce the recombinant DNA molecules of the
CC invention. These comprise a genetic construct consisting of a promoter
CC directing temporal and/or spatial gene expression in plant seed
CC operatively linked to a cytokinin modulating gene. The recombinant DNA
CC molecules are useful for producing fertile, transgenic plants capable of
CC regulated expression of a cytokinin modulating gene in developing seeds.

CC They are also useful for improving stress tolerance and yield stability
CC in plants. The preferential expression of recombinant DNA molecules of
CC the invention occurs about 14-25 days after pollination. The transgenic
CC plants thus produced have enhanced levels of cytokinin expression exhibit
CC improved seed size, decreased tip kernel abortion and increased seed set
CC during unfavourable environmental conditions

XX Sequence 721 BP, 182 A, 176 C, 191 G, 172 T, 0 U, 0 Other;

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 1,17e-132 | Length: | 721 |
| Score: | 1230.00 | Matches: | 239 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-10-817-483-2 (1-239) x AAC6514 (1-721)

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OY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 2 ATGATCTACGCTCTAATTTTCGGTCCAACTTGACAGGAAGACATCGACTGCGACT 61
OY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysGlyProGln 40
DB 62 CTGGCCGACAGACGCGCTCCCAAGTCTCTCGCTCGATCGCGGTCCAATGCTGCTTCAA 121
OY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB 122 CTATCAACCGGAAGGGGCGACCAACAGTGGAAAGACTGAAGAACACATCGTCTGTAC 181
OY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB 182 CTGATGATCGCCCTTTGGTAAAGGATATCATTAACAGCAAGCTCATGAACGGCTC 241
OY 81 IleAlaGlnValHisAsnHisGlnAlaLysGlyLysGlyLeuGluGluGlySerIle 100
DB 242 ATTCGGAGAGTGCAAAATCAACAGGCGCAAGCGGCTTATCTTGAGGAGATCTATC 301
OY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTPAsnAlaAspPheArgTrpHisIle 120
DB 302 TCGTGTCTCAGGTGATGCGCAAGTCTTATTGMAACGGCATTTTCGTTGGCATATT 361
OY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
DB 362 ATTGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGGTGCCAAGCCAGACTTAA 421
OY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 422 CAGATGTTACGCCCTCTGCAAGTCTTCTATTATCCAAAGATTGTTCAACTTTGGAGG 481
OY 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 482 GAGCTCGGCTGAGGCGCCATCTGGAAGGATCGATGGATATCATATGCTCTATTATT 541
OY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 542 GCTACCAAGAACCAATCATCGCCGATATGCTATTGCAAGCTGACGACGATATGAGAT 601
OY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
DB 602 AAATTGATTCACGGATATGCTCAGAGATTCTTAATCCATGCGCGTCGACAGGAACAGAA 661
OY 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGluGlyProProPheArgMet 239
DB 662 TTCCTTTGGTGGGCGACAGCTGTCAAGGCTTTGAAGACCACTTTGCAATG 718
```

RESULT 3

ACF58155
ID ACF58155 standard; cDNA; 723 BP.

XX ACF58155;
XX

DT 15-JAN-2004 (first entry)

XX Z. mays isopenentenyl transferase encoding cDNA.

DE Z. mays isopenentenyl transferase; gene, ss.

XX isopenentenyl transferase; gene, ss.

XX Zea mays.

XX Key Location/Qualifiers

FT CDS 1..723

FT /tag= a

FT /product= "isopenentenyl transferase"

XX WO2003087313-A2.

XX 23-OCT-2003.

XX 08-APR-2003; 2003WO-US010544.

XX 08-APR-2002; 2002US-0370796P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Zinselmeier C, Helentjaris TG;

XX WPI; 2003-845315/78.

XX P-PSDB; ABR61587.

PT Enhancing silk exertion in a Zea mays plant under stress, relative to a

PT non-transformed Zea mays plant under stress by transforming the plant or

PT its ancestor with a construct comprising a silk-specific or silk-

PT preferred promoter.

PS Claim 2; Page 67-68; opp; English.

CC The invention relates to enhancing silk exertion in a Zea mays plant

CC under stress, relative to a non-transformed Zea mays plant under stress.

CC The method involves transforming the plant or its ancestor with a

CC construct comprising a silk-specific or silk-preferred promoter operably

CC linked to a polynucleotide encoding a polypeptide that increases cell

CC division. The present sequence represents a cDNA encoding a Z. mays

CC isopenentenyl transferase, a polypeptide involved in cell division

XX Sequence 723 BP, 181 A, 176 C, 192 G, 174 T, 0 U, 0 Other;

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 1,17e-132 | Length: | 723 |
| Score: | 1230.00 | Matches: | 239 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 10 | Gaps: | 0 |

US-10-817-483-2 (1-239) x ACF58155 (1-723)

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OY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 1 ATGATCTACGCTCTAATTTTCGGTCCAACTTGACAGGAAGACATCGACTGCGACT 60
OY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysGlyProGln 40
DB 61 CTGGCCGACAGACGCGCTCCCAAGTCTCTCGCTCGATCGCGGTCCAATGCTGCTTCAA 120
OY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB 121 CTATCAACCGGAAGGGGCGACCAACAGTGGAAAGACTGAAGAACACATCGCTGTAC 180
OY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB 181 CTGATGATCGCCCTTTGGTAAAGGATATCATTAACAGCAAGCTCATGAACGGCTC 240
OY 81 IleAlaGlnValHisAsnHisGlnAlaLysGlyLysGlyLeuGluGluGlySerIle 100
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Db 241 ATTCGGAGGTGACAAATCAGAGGCCAAAGCGGGCTTATTTGAGGAGATCTATTC 300
Qy 101 SerleuLeuAryGySmelAglInserAryTyrTpaAnaalAaspPheAryTyrHisIle 120
Db 301 TCGTTGCTCAGGTGATGATGCCCAAGTCTTATTGGAACGGGAGATTTTGGTGGCATATT 360
Qy 121 IleArgAnGluLeuAlaAspGluGluSerPheMetSerValAlaIleThrArgValIys 140
Db 361 ATTGGCAACGAGTTAGCAGACGAGAGAGCTTACAGACGGCGCCAAACCAAGTTAAG 420
Qy 141 GlnMetLeuAryGProSerAglIleuSerIleIleGlnGluLeuValGlnLeuTyrArg 160
Db 421 CAGATTGTTACCCCTCTTCAGAGTCTTTCTATTATCCAGAGTTGCTTCACTTTGAGG 480
Qy 161 GluProAryLeuAryGProIleuGluGluIleAspGlyTyrArgTyrAlaLeuIleuPhe 180
Db 481 GAGCTCGGCTGAGAGCCCATATGGAAGGATTCGATATTCGATATGCCCTGTATT 540
Qy 181 AlAthrGlnAnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 541 GCTACCCCAACCAAGATCAGCCCGCATATGCTATTGTCAGCTCGACGCAATATGAGAA 600
Qy 201 LysLeuIleHISGlyIleAlaGlnGluPheLeuIleHISAlaArgArgGlnGluIleIys 220
Db 601 AAATTGATTCCAGGTATCGCTCAGAGTTTCTTAATCCATGCGCGCTCGACAGAAACAGAA 660
Qy 221 PheProLeuValGlyAlaThrAlaValGluIleAphGlnGlyProProPheArgMet 239
Db 661 TTCCCTTGGTGGGGCGACAGCTGTGCAAGGTTTGAAGGCCACCATTCGAATG 717

RESULT 4
ADT92127
ID ADT92127 standard; DNA; 1919 BP.

AC ADT92127;
XX 13-JAN-2005 (first entry)
DT
XX
XX A. tumefaciens isopentenyl transferase (ipt) encoding DNA.
XX
XX Ipt; transgenic; plant; cytokinin; female reproduction;
XX isopentenyl transferase; plant breeding; gene; ds.
XX
XX Agrobacterium tumefaciens.
XX
XX Key Location/Qualifiers
XX CDS 690..1409
XX FT /*tag= a
XX FT /product= "ipt"
XX
XX WO2004090143-A2.
XX
XX 21-OCT-2004.
XX
XX 02-APR-2004; 2004WO-US010064.
XX
XX 04-APR-2003; 2003US-0460718P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Haben JE, Zinselmeier C, Tomes DT, Abbitt SE, Helentjaris TG;
XX Niu X;
XX
XX WPI; 2004-748771/73.
XX P-PSDB; ADT92128.
XX GENBANK; X14410.
XX
XX Producing transgenic plants capable of regulated expression of cytokinin-
XX modulating gene comprises transformation of plant cells with a genetic
XX construct capable of temporally- or spatially-regulated expression of
XX cytokinin modulating gene.

PS Claim 37; SEQ ID NO 1; 157bp; English.

XX The invention relates to producing transgenic plants capable of the
CC regulated expression of a cytokinin-modulating gene in developing seed or
CC related female reproductive tissue. The method involves transformation of
CC plant host cells with a genetic construct capable of temporally- or
CC spatially-regulated expression of a cytokinin modulating gene in
CC developing seed or related female reproductive tissue, and regenerating
CC and recovering the transgenic plants. The transformation is carried out
CC by electroporation, PEG poration, particle bombardment, silicon fiber
CC delivery, microinjection, or Agrobacterium-mediated transformation. The
CC genetic construct comprises a promoter directing temporal or spatial gene
CC expression in developing seed or related female reproductive tissue.
CC operably linked to a cytokinin-modulating gene. The promoter is selected
CC from 2ag2.1, zap, tbi, eep1, eep2, F3.7, ttxH, Zm40, ESR, PCNA2, lcc1,
CC ZmCkx1-2, ZmCkx2, ZmCkx4, or ZmCkx5. The cytokinin-modulating
CC gene is selected from genes encoding cytokinin biosynthetic enzymes,
CC cytokinin catabolic enzymes, cytokinin catabolic enzyme antagonists, or
CC cytokinin biosynthetic enzyme agonists. The method is useful for
CC producing transgenic plants having enhanced cytokinin activity.
CC Transgenic plants exhibit useful characteristics including improved seed
CC size, decreased tip kernel abortion, or stability of yield. The probes
CC that hybridize to cytokinin metabolic enzyme polynucleotide sequences are
CC useful as molecular markers in breeding programs. The inhibitors to the
CC polypeptides are useful for modulating the activity and/or expression of
CC the polypeptides. The products, compositions, processes, and methods
CC above are useful for research, biological, and agricultural purposes. The
CC present sequence represents a DNA encoding an A. tumefaciens isopentenyl
CC transferase (ipt) enzyme.
XX

SQ Sequence 1919 BP; 533 A; 378 C; 441 G; 567 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 4.7e-132 | Length: | 1919 |
| Score: | 1230.00 | Matches: | 239 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 13 | Gaps: | 0 |

US-10-817-483-2 (1-239) x ADT92127 (1-1919)

Qy 1 MetAspLeuAryGluIlePheGlyProThrCySerThrGlyIleThrSerThrAlaIleAla 20
Db 690 ATGAGTCTACGCTTAATTTGTCCTCACTTGCACAGAGAAAGAAATCAGCTGCACTACT 749
Qy 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCySerProGln 40
Db 750 CTGGCCACGACGATCGCTCCAGTCTCTCGCTCGATCGCGTCCAAATGCTGCTCA 809
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuIleuIleuIleuIleuIleuIleu 60
Db 810 CTATCAACCGGAGCGGGCGACCAACAGTGAAGAACTGAAGAAAGCACTCGTCTGAC 869
Qy 61 LeuAspAspArgProLeuValIleuGlyIleIleThrAlaIleuIleuIleuIleuIleu 80
Db 870 CTGATGATCGCCCTTGGTAAAGGATATCTTACAGCAAGCAAGCTCAAGACGGCTC 929
Qy 81 IleAlaGluValHisAsnHisGluAlaIleuIleuIleuIleuIleuIleuIleuIleuIleu 100
Db 930 ATTCGGAGGTGACAAATCAGAGGCCAAAGCGGGCTTATTTGAGGAGATCTATTC 989
Qy 101 SerleuLeuAryGySmelAglInserAryTyrTpaAnaalAaspPheAryTyrHisIle 120
Db 990 TCGTTGCTCAGGTGATGATGCCCAAGTCTTATTGGAACGGGAGATTTTGGTGGCATATT 1049
Qy 121 IleArgAnGluLeuAlaAspGluGluSerPheMetSerValAlaIleThrArgValIys 140
Db 1050 ATTGGCAACGAGTTAGCAGACGAGAGAGCTTACAGACGGCGCCAAACCAAGTTAAG 1109
Qy 141 GlnMetLeuAryGProSerAglIleuSerIleIleGlnGluLeuValGlnLeuTyrArg 160

DB 1110 CAGATGTTACGCCCTCTGACGCTTTCTATTATCCAAAGTTGGTTCAACTTTGGAGG 1169
QY 161 GIUProArGLeuArGLProIleLeuGLuGIYIleAspGIYTYrArgTYrAlaLeuPhe 180
DB 1170 GAGCTCGGCTGAGGCCCATCTAGTGAAGGATCGATGATATCATGATATGCCCTGCTATT 1229
QY 181 A1aThrGlnAangInIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 1230 GCTACCCAGAAACCAATCATCGCCCATATGCTATTGTCAGCTCGACGAGATATGAGAAAT 1289
QY 201 LysLeuIleHISGLYIleAlaGlnGluPheLeuIleHISAlaArgArgGlnGluGlnIys 220
DB 1290 AAATTGATTCAAGGATGCTCAGAGATTCTTAATCTCATGCGCGTCGACAGAAACAGAA 1349
QY 221 PheProLeuValGIYAlaThraIaValaGlnaIaPheGluGIYProProPheArgMet 239
DB 1350 TTCCTTTGGTGGGCGGACAGCTGTCCAGAGCTTTGAAGACCAACATTTCGAATG 1406

RESULT 5
AAC86508 ID AAC86508 standard; DNA; 2722 BP.
AC AAC86508;
AC AAC86508;
DT 19-MAR-2001 (first entry)
XX
DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.
XX
KW temporal gene expression; spatial gene expression; plant seed;
KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KW ipt; ss.

OS Synthetic.
OS Zea mays.
OS Agrobacterium tumefaciens.
OS Solanum tuberosum.
XX WO200063401-A1.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000MO-US009943.
XX
PR 16-APR-1999; 99US-0129844P.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Haben JE, Zinselmeier C, Tomes D;
XX
DR WPI: 2000-672743/65.
XX
PT Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.
XX
PS Disclosure; Page 70-71; 76pp; English.

CC The present sequence represents a recombinant DNA molecule of the
CC invention. It comprises, in this order, a maize promoter, an
CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a Solanum
CC tuberosum terminator. The DNA molecules of the invention comprise a
CC genetic construct consisting of a promoter directing temporal and/or
CC spatial gene expression in plant seed operatively linked to a cytokinin
CC modulating gene. The recombinant DNA molecules are useful for producing
CC fertile, transgenic plants capable of regulated expression of a cytokinin
CC modulating gene in developing seeds. They are also useful for improving
CC stress tolerance and yield stability in plants. The preferential
CC expression of recombinant DNA molecules of the invention occurs about 14-
CC 25 days after pollination. The transgenic plants thus produced have
CC enhanced levels of cytokinin expression exhibit improved seed size,
CC decreased tip kernel abortion and increased seed set during unfavourable
CC environmental conditions

XX
SQ Sequence 2722 BP; 732 A; 610 C; 619 G; 761 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 7,736-132 Length: 2722
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-817-483-2 (1-239) x AAC86508 (1-2722)

QY 1 MetaAspLeuArGLeuIlePheGIYProThrCysThrGIYThS-ThrThraIleAla 20
DB 1525 ATGATCTACGCTATATTTTCGGTCCACTTGACAGAAAGACATCGACTCGATAGCT 1584
QY 21 LeuAlaGlnGlnInThrGIYLeuProValLeuSerLeuAspArgValGInCysCysProGln 40
DB 1585 CTGGCCAGACAGACTGGCTCCCAAGTCTCTCGCTCGATCGCGTCCAATGCTGCTCA 1644
QY 41 LeuSerThrGIYSerGIYArgProThrValaGlnGluLeuYSGLYThrThrArgLeuTYr 60
DB 1645 CTATCAACCGAAGGCGGCGACCAACATGGAAGACTGAAGAACACATCTGCTGTAC 1704
QY 61 LeuAspAspArgProLeuValIysGLYIleIleThraIaIysGlnaIaHISGluArgLeu 80
DB 1705 CTGATGATCGCCCTTGGTAAAGGATATTCATTACAGCAAGCATCATGACGGCTC 1764
QY 81 IleAlaGluValHISAsnHISGlnAlaIysGLYIleLeuGlnGluGIYSerIle 100
DB 1765 ATTCGAGAGGTGCACAACTACAGAGCCCAAGCGGGCTTATTCCTTGAAGAGATCTATC 1824
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTYrTPAAnaIaAspPheArgTTPHISile 120
DB 1825 TCGTTCTCAGGTGATGATGCCGCAAGTCTTATTTGAACCGGATTTTCGTTGGCATATT 1884
QY 121 IleArgAangIuLeuAlaAspGlnGluSerPheMetSerValaIaIysThrArgValIys 140
DB 1885 ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCTGAGCCAAACAGATTAAAG 1944
QY 141 GlnMetLeuArgProSerAlaGIYLeuSerIleIleGlnGluLeuValGlnLeuTTPArg 160
DB 1945 CAGATGTTACGCCCTCTGACAGCTCTTCTATTTATCAAGAGTTGGTCACTTTGGAGG 2004
QY 161 GIUProArGLeuArGLProIleLeuGLuGIYIleAspGIYTYrArgTYrAlaLeuPhe 180
DB 2005 GAGCTCGGCTGAGGCCCATCTGGAAGGATCGATGATATCATATGCCCTGCTATT 2064
QY 181 A1aThrGlnAangInIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 2065 GCTACCCAGAAACCAATCATCGCCCATATGCTATTGTCAGCTCGACGAGATATGAGAAAT 2124
QY 201 LysLeuIleHISGLYIleAlaGlnGluPheLeuIleHISAlaArgArgGlnGluGlnIys 220
DB 2125 AAATTGATTCAAGGATGCTCAGAGATTCTTAATCTCATGCGCGTCGACAGAAACAGAA 2184
QY 221 PheProLeuValGIYAlaThraIaValaGlnaIaPheGluGIYProProPheArgMet 239
DB 2185 TTCCTTTGGTGGGCGGACAGCTGTCCAGAGCTTTGAAGACCAACATTTCGAATG 2241

RESULT 6
AAC86507 ID AAC86507 standard; DNA; 2722 BP.
AC AAC86507;
AC AAC86507;
DT 19-MAR-2001 (first entry)
XX
DE DNA comprising a barley promoter and Agrobacterium ipt gene.
XX
KW temporal gene expression; spatial gene expression; plant seed;
KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;

KM yield stability; tip kernel abortion; seed set; isopentenyl transferase;
 KM ipc; ss.
 XX
 OS Synthetic.
 OS Hordeum vulgare.
 OS Agrobacterium tumefaciens.
 OS Zea mays.
 PN WO20063401-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 13-APR-2000; 2000WO-US009943.
 XX
 PR 16-APR-1999; 99US-0129844P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Habben JE, Zinselmeier C, Tomes D;
 XX
 DR WPI; 2000-672743/65.
 XX
 PT Novel recombinant DNA construct useful for producing transgenic plants
 PT having enhanced levels of cytokinin expression, improved stress tolerance
 PT and yield stability.
 XX
 PS Disclosure; Page 69-70; 76pp; English.
 XX
 CC The present sequence represents a recombinant DNA molecule of the
 CC invention. It comprises, in this order, a barley promoter, an
 CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
 CC terminator. The DNA molecules of the invention comprise a genetic
 CC construct consisting of a promoter directing temporal and/or spatial gene
 CC expression in plant seed operatively linked to a cytokinin modulating
 CC gene. The recombinant DNA molecules are useful for producing fertile,
 CC transgenic plants capable of regulated expression of a cytokinin
 CC modulating gene in developing seeds. They are also useful for improving
 CC stress tolerance and yield stability in plants. The preferential
 CC expression of recombinant DNA molecules of the invention occurs about 14-
 CC 25 days after pollination. The transgenic plants thus produced have
 CC enhanced levels of cytokinin expression exhibit improved seed size,
 CC decreased tip kernel abortion and increased seed set during unfavourable
 CC environmental conditions
 CC
 XX
 SQ Sequence 2722 BP; 732 A; 610 C; 619 G; 761 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 7.73e-132 Length: 2722
 Score: 1230.00 Matches: 239
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0
 US-10-817-483-2 (1-239) x AAC86507 (1-2722)
 QY 1 MetAspLeuAArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
 DB 1525 ATGATCTACGCTCTAATTTCGCTCCAACTTGCAAGGAAAGACATCGACTCGCATCT 1584
 QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
 DB 1585 CTGGCCGACAGACTGGCTCCCACTCCCTGCTCGATCGGCTCAATGCTGCTCA 1644
 QY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
 DB 1645 CTATCAACCGAAGCGGCGGACCAACAGTGGAGAAGACTGAAAGAACACTGCTGTGAC 1704
 QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu 80
 DB 1705 CTTGATGATCGCCCTTTGGTAAAGGGTATCATTAACGCAAGCATCATGAACGGCTC 1764
 QY 81 IleAlaGluValHisAsnHisGlnAlaLysGlyGlyLeuIleLeuGlnGlyGlySerIle 100

DB 1765 ATTCGGAGGGTGCAATTCACGAGGCCCAAGCGGCTTATTCTTAGGGAGATCTATC 1824
 QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
 DB 1825 TCGTTGCTCAGGTGCATGCGCAAAAGTCATTATGGAACGGGATTTTCGTGGCATATTT 1884
 QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
 DB 1885 ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGCGCAAGACCAAGATTAA 1944
 QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
 DB 1945 CAGATGTTACGCCCTCTGACGGTCTTTCTATATTCAGAGCTTGTTCACTTTGGAGG 2004
 QY 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
 DB 2005 GAGCCTGGCTGAGGCCCATCTGGAAGGATTCATGGAATATGCTATGCCCTGCTATTT 2064
 QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
 DB 2065 GCTACCCAGAACACGATCACGCCGATATGCTATTGACGCTCGACGACGATATGGAAT 2124
 QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluIle 220
 DB 2125 AAATTGATTCACGGTATCGCTCAGAGATTCTATTCATGCGCGCTCCACAGGAACAGAA 2184
 QY 221 PheProLeuValGlyAlaThrAlaValAlaGlnLeuGluGlyProProPheArgMet 239
 DB 2185 TTCCCTTGTGGGCGGACAGCTGCGAAGCGTTTGAAGACCAACCATTTGCAATG 2241
 RESULT 7
 AAC86511
 ID AAC86511 standard; DNA; 3017 BP.
 AC AAC86511;
 DT 19-MAR-2001 (first entry)
 XX
 DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.
 XX
 KW temporal gene expression; spatial gene expression; plant seed;
 KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
 KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
 KW ipc; ss.
 XX
 OS Synthetic.
 OS Zea mays.
 OS Agrobacterium tumefaciens.
 PN WO20063401-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 13-APR-2000; 2000WO-US009943.
 XX
 PR 16-APR-1999; 99US-0129844P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Habben JE, Zinselmeier C, Tomes D;
 XX
 DR WPI; 2000-672743/65.
 XX
 PT Novel recombinant DNA construct useful for producing transgenic plants
 PT having enhanced levels of cytokinin expression, improved stress tolerance
 PT and yield stability.
 XX
 PS Disclosure; Page 72-73; 76pp; English.
 XX
 CC The present sequence represents a recombinant DNA molecule of the
 CC invention. It comprises, in this order, a maize promoter, an
 CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize

CC terminator. The DNA molecules of the invention comprise a genetic
 CC construct consisting of a promoter directing temporal and/or spatial gene
 CC expression in plant seed operatively linked to a cytokinin modulating
 CC gene. The recombinant DNA molecules are useful for producing fertile,
 CC transgenic plants capable of regulated expression of a cytokinin
 CC modulating gene in developing seeds. They are also useful for improving
 CC stress tolerance and yield stability in plants. The preferential
 CC expression of recombinant DNA molecules of the invention occurs about 14-
 CC 25 days after pollination. The transgenic plants thus produced have
 CC enhanced levels of cytokinin expression exhibit improved seed size,
 CC decreased tip kernel abortion and increased seed set during unfavourable
 CC environmental conditions

XX
 SQ Sequence 3017 BP; 865 A; 679 C; 622 G; 851 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 8_95e-132 | Length: | 3017 |
|------------------------|-----------|---------------|------|
| Score: | 1230.00 | Matches: | 239 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-10-817-483-2 (1-239) X AAC86511 (1-3017)

QY 1 MetAapLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIleAla 20
 DB 1408 ATGGATCTACGCTAATTTTCGGTCCACCTTGACAGAAAGCATCGACTCGATAGCT 1467
 QY 21 LeuAlaGlnGlnThGlyLeuProValLeuSerLeuAspArgValGlnCysAspProGln 40
 DB 1468 CTTGCCACACAGCTGGCTCCAGTCTCTGCTGCTGATGGCTCAATGCTGCTCTCA 1527
 QY 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyThrThraArgLeuYr 60
 DB 1528 CTATCAACCGGAAGGGGGGACCAACAGTGAAGAACTGAAGAAAGCATGCTGCTGATC 1587
 QY 61 LeuAspAspArgProLeuValLysGlyIleIleThraLysGlnAlaHisGlnArgLeu 80
 DB 1588 CTTGATGATGCGCTTTGTTAAAGGATATCATTAACGACCAAGCTCATGACCGCTC 1647
 QY 81 IleAlaGlnValHisAsnHisGlnAlaLysGlyLysLeuIleLeuGlnGlySerIle 100
 DB 1648 ATTTGGAGAGTGCACATACAGAGGCAAGGGGCTTAATCTTGAGGAGATCTATC 1707
 QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
 DB 1708 TCGTTGCTCAGGTGATGGCGCAAGTCTTATTGGAACGCCGATTTTCTTGCGCATATT 1767
 QY 121 IleArgAsnGlnLeuAlaAspGlnGlnSerPheMetSerValAlaLysThraArgValLys 140
 DB 1768 ATTCACCAAGAGTGTGACAGACAGAGAGAGCTTCATGAGCGTGGCCAAAGACAGAGTTAAG 1827
 QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
 DB 1828 CAGATGTTAGGCCCTCTGCAAGTCTTTATTATTCAGAAAGTGGTTCAACTTGGAGAG 1887
 QY 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuPhe 180
 DB 1888 GAGCCTCGGCTAGAGCCCATATCTGGAAGGATCGATGATATCGATATCCCTGCTATT 1947
 QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGlnAsn 200
 DB 1948 GCTACCCAGAACACAGATCAGCCCGCATATGCTATTCAGACTCGACCAATATGAGAAAT 2007
 QY 201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLys 220
 DB 2008 AATATGATTCACGGATTCCTCAGAGAGTTCTTAATCCATGCGCTGACAGAAACGAA 2067
 QY 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
 DB 2068 TTCCTTTGTTGGTGGGGCGACAGCTGTGAAAGGCTTTGAAGAGACCAACATTTGATG 2124

RESULT 8

AAC86506
 ID AAC86506 standard; DNA; 5622 BP.

XX AAC86506;

XX 19-MAR-2001 (first entry)

DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.

XX temporal gene expression; spatial gene expression; plant seed;

KM cytokinin modulating gene; transgenic plant; seed size; stress tolerance;

KM yield stability; tip kernel abortion; seed set; isopentenyl transferase;

XX ipt; ss.

XX Synthetic.

OS Zea mays.

OS Agrobacterium tumefaciens.

XX WO200063401-A1.

XX 26-OCT-2000.

XX 13-APR-2000; 2000WO-US009943.

XX 16-APR-1999; 99US-0129844P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Haben JE, Zinselmeier C, Tones D;

XX WPI, 2000-672743/65.

XX Novel recombinant DNA construct useful for producing transgenic plants

PT having enhanced levels of cytokinin expression, improved stress tolerance

PT and yield stability.

XX Disclosure; Page 67-69; 76pp; English.

XX The present sequence represents a recombinant DNA molecule of the

CC invention. It comprises, in this order, a maize promoter, an

CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize

CC terminator. The DNA molecules of the invention comprise a genetic

CC construct consisting of a promoter directing temporal and/or spatial gene

CC expression in plant seed operatively linked to a cytokinin modulating

CC gene. The recombinant DNA molecules are useful for producing fertile,

CC transgenic plants capable of regulated expression of a cytokinin

CC modulating gene in developing seeds. They are also useful for improving

CC stress tolerance and yield stability in plants. The preferential

CC expression of recombinant DNA molecules of the invention occurs about 14-

CC 25 days after pollination. The transgenic plants thus produced have

CC enhanced levels of cytokinin expression exhibit improved seed size,

CC decreased tip kernel abortion and increased seed set during unfavourable

CC environmental conditions

XX
 SQ Sequence 5622 BP; 1546 A; 1295 C; 1189 G; 1592 T; 0 U; 0 Other;

Alignment Scores:

| Pred. No.: | 2_17e-131 | Length: | 5622 |
|------------------------|-----------|---------------|------|
| Score: | 1230.00 | Matches: | 239 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-10-817-483-2 (1-239) X AAC86506 (1-5622)

QY 1 MetAapLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIleAla 20
 DB 1525 ATGGATCTACGCTAATTTTCGGTCCACCTTGACAGAAAGCATCGACTGCGATAGCT 1584
 QY 21 LeuAlaGlnGlnThGlyLeuProValLeuSerLeuAspArgValGlnCysAspProGln 40
 |||

| | | | |
|----------|--|---|------|
| Db | 1585 | CTTGCCAGCAGACGACTGGCTCCAGTCTCTTCGCTCGATCGGCTCAATGCTGCTCTCA | 1644 |
| Qy | 41 | LeuSerThrglySerGlyYargProThrValGluLeuGlySerGlyThrThrArgLeuTyr | 60 |
| Db | 1645 | CTATCAACCCGGAACCGGGCGACCAACAGTGGAAAGAACTGAAAGCACTGCTTGAC | 1704 |
| Qy | 61 | LeuAspAspArgProLeuValValGlyGlyLeileIleThrAlaValGlnAlaHisGluArgLeu | 80 |
| Db | 1705 | CTTGATGATGCCCTTCCTTGGTAAAGGTATCTTACAGCCAAAGCAAGCTCATGAACGGCTC | 1766 |
| Qy | 81 | IleAlaGluValHisAsnHisGluAlaValGlyGlyLeuIleLeuGluGlyGlySerIle | 100 |
| Db | 1765 | ATTGCGGAGGTGCACAATCAACAGAGGCCAAAGCGGGCTTATTCTTGAGGAGGATCTATAC | 1824 |
| Qy | 101 | SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle | 120 |
| Db | 1825 | TCGTGTCTCAGAGTGATGGCCGCAAAAGTGTATTGGAAAGCGGATTTTCGTGGCATATT | 1884 |
| Qy | 121 | IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaIleThrArgValIys | 140 |
| Db | 1885 | ATTGCGAACGAGTTATAGCAGACGAGGAGAGCTTCATGACGCGTGGCCAAACCAAGTTAAG | 1944 |
| Qy | 141 | GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTyrArg | 160 |
| Db | 1945 | CAGATGTTACCCCTTCGACAGGCTTCTTCTATTACCAAGAGTTGGTCAACTTGGAGGG | 2004 |
| Qy | 161 | GluProArgLeuArgProIleLeuGluGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe | 180 |
| Db | 2005 | GAGCTCGGCTGAGAGGCCCATCTAGGAAAGGATCGATGATATCGATATAGCCCTGTAATT | 2066 |
| Qy | 181 | AlaThrGlnAsnGlnIleIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn | 200 |
| Db | 2065 | GCTACCCCAAGAACCGAGATCACCCCGCATATGCTATTGCAGCTCGACGACAGATATGAGGAAT | 2124 |
| Qy | 201 | LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnIys | 220 |
| Db | 2125 | AAATTGATTCAAGGTATGCTCAGAGATTCTTAATCCATGCGCGTCGACAGAACAGAA | 2186 |
| Qy | 221 | PheProLeuValIleGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet | 239 |
| Db | 2185 | TTCCCTTTGTGTGGGGCGACAGACTGTGAAAGGTTGAAGGCCACCATTTGCAATG | 2241 |
| RESULT 9 | | | |
| ID | AD563280 | standard; cDNA; 720 BP. | |
| XX | AD563280; | | |
| AC | | | |
| XX | 02-DEC-2004 (first entry) | | |
| DT | | | |
| XX | Bacterial polynucleotide #15267. | | |
| DE | | | |
| XX | | | |
| KM | Recombinant DNA construct; transformed plant; improved plant property; | | |
| KM | cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic; | | |
| KM | pathogen tolerance; pest tolerance; plant disease resistance; | | |
| KM | cell cycle pathway modification; plant growth regulator; | | |
| KM | homologous recombination; seed oil yield; protein yield; carbohydrate; | | |
| KM | nitrogen; phosphorus; photosynthesis; lignin; galactomannan; | | |
| KM | bacterial polynucleotide; gene; ss. | | |
| XX | | | |
| OS | Bacteria. | | |
| XX | | | |
| PN | US2003233675-A1. | | |
| XX | | | |
| PD | 18-DEC-2003. | | |
| XX | | | |
| PF | 20-FEB-2003; 2003US-00369493. | | |
| XX | | | |
| PR | 21-FEB-2002; 2002US-0360039P. | | |
| XX | | | |
| PA | (CAOY/) CAO Y. | | |
| PA | (HINK/) HINKLE G J. | | |
| PA | (SLAT/) SLATER S C. | | |

| | |
|--|---|
| PA | (CHEN)/ CHEN X. |
| PA | ((GOLD)) GOLDMAN B S. |
| PI | Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS; |
| XX | |
| XX | WP1; 2004-061375/06. |
| DR | |
| XX | |
| PT | New recombinant DNA construct comprising a promoter positioned to provide |
| PT | for expression of a polynucleotide encoding a polypeptide from a |
| PN | microbial source, useful for producing plants with improved properties. |
| PS | |
| XX | |
| XX | Claim 1; SEQ ID NO 38954; 122bp; English. |
| CC | The invention relates to a recombinant DNA construct comprising a |
| CC | promoter functional in a plant cell, where the promoter is positioned to |
| CC | provide for expression of a polynucleotide encoding a polypeptide from a |
| CC | microbial source. The invention also relates to a transformed plant |
| CC | comprising the recombinant DNA construct and a method of producing a |
| CC | transformed plant having an improved property. The plant is a crop plant |
| CC | such as maize or soybean. The method of producing a transformed plant |
| CC | having an improved property comprises transforming a plant with the |
| CC | recombinant DNA construct and growing the transformed plant, where the |
| CC | polynucleotide or polypeptide is useful for improving plant properties. |
| CC | The recombinant DNA construct is useful for producing plants with |
| CC | improved plant properties, e.g. improved cold, heat or drought tolerance, |
| CC | tolerance to herbicides, extreme osmotic conditions, pathogens or pests, |
| CC | increased resistance to plant disease, better growth rate by modification |
| CC | of the cell cycle pathway with plant growth regulators, increased rate of |
| CC | homologous recombination, modified seed oil or protein yield and/or |
| CC | content, improved yield by modification of carbohydrate, nitrogen or |
| CC | phosphorus use and/or uptake, by modification of photosynthesis or by |
| CC | providing improved plant growth and development under at least one stress |
| CC | condition, improved lignin production or improved galactomanan |
| CC | production. This sequence represents a bacterial polynucleotide used in |
| CC | the scope of the invention. Note: The sequence data for this patent did |
| CC | not form part of the printed specification but was obtained in electronic |
| CC | format from USPTO at seqdata.uspto.gov/sequence.html. |
| XX | |
| SQ | Sequence 720 BP; 182 A; 166 C; 197 G; 175 T; 0 U; 0 Other; |
| Alignment Scores: | |
| Pred. No.: | 1,11e-114 Length: 720 |
| Score: | 1075.00 Matches: 206 |
| Percent Similarity: | 93.7% Conservative: 18 |
| Best Local Similarity: | 86.2% Mismatches: 15 |
| Query Match: | 87.4% Indels: 0 |
| DB: | Gaps: 0 |
| US-10-817-483-2 (1-239) x ADS63280 (1-720) | |
| OY | 1 MetaspLeuAgtgLeuIlePheGlyProThrCyThrGlyVtHserThraIaiIeaJa 20 |
| Db | 1 ATGGATCTCGCCTCAATTTCGATCCAATTGCACAGGAACAACGTGCAGCCGGTAGCT 60 |
| OY | 21 LeuIIaGInGInThGlyLeuProValIleuSerLeuAspArgValGlnCyCspProGIn 40 |
| Db | 61 CTGGCCACGACACTGGGCTTCAAGTCCTTGCTCGATCGGGATCCAAATGTGTCTCAK 120 |
| OY | 41 LeuSerThrgIySergIyArGProThrValGInGuIuLeuLySglYThrThraIrgLeuTyR 60 |
| Db | 121 CTGTCAACCGGAAGCGACGACCAACAGTGGAAAGAACTGAAGAAGAACGAGCGCTATAC 180 |
| OY | 61 LeuAspAParAgProLeuValIysGlyIleIetThraIAlvGlnAlaHisGluAgtLeu 80 |
| Db | 181 CTTGATGATCGGCCCTCTGCTGAAGGGATCATCGGACGCCAACCAAGCTCATGAAGGCTG 240 |
| OY | 81 IleaIaGIVaIHiaSasnHisGluAlaLySglYtyleuIleLeuGInuIyGlySerIle 100 |
| Db | 241 ATGGGGAGAGGTATAATTATTCAGGCCCAAGCGCGGCTTATTCTTCAGGAGAGATTAAC 300 |
| OY | 101 SerLeuLeuAryCYMeLalagInSerArgrYTrTPasnaIaASPPhearGrTrphisIle 120 |
| Db | 301 TCCTTGCTCAAGTGCATGGCCGAAGAAGAGTATTAATGAGAGCGGATTTTCGTTGGCAATAT 360 |

QY 121 IleaAgAngluLeuAlaAspGluSerPheMetSerValAlaIleThrArgValLys 140
DB 361 ATTCGCCAGAGTTAGCAGACGAAAGACCTTCATGAACTGGCCAAAGCCAGATTAAAG 420
QY 141 GlnMetLeuArgProSerIleGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACGCCCTGCTGCAGGCCCTTCTATTATTCAGAAAGTTGGATTGTTGGAAA 480
QY 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 461 GAGCTTCGGCTCAGGCCCACTACTGAAAGATCGATGATATCGATATCCATGTTGTTT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 541 GCTACCCAGAACCAAGATCCATCCGATATGCTATTGACAGCTTGACGACAGATATGGAGGAT 600
QY 201 LysLeuIleHisGlyTyrIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnGlnLys 220
DB 601 AAGTTGATTTCATGGAGATCGCTCAGAGATGTCATTCATTCATGACGCCGACAGAACAGAA 660
QY 221 PheProLeuValGlyValAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
DB 661 TTCCCTCAGATTACGCGACGCCGCTTACGACGATTGCAAGTTCATTCATTCGGAATG 717
RESULT 10
ADS62464
ID ADS62464 standard; cDNA; 720 BP.
XX
AC ADS62464;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #14451.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
bacterial polynucleotide; gene; ss.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI, 2004-061375/06.
DR
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 36138; 122bp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant

CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX

SQ Sequence 720 BP; 181 A; 166 C; 198 G; 175 T; 0 U; 0 Other;

Alignment Scores: 1,116-114 Length: 720
Pred. No.: 1075.00 Matches: 206
Score: 93.74 Conservative: 18
Percent Similarity: 86.24 Mismatches: 15
Best Local Similarity: 87.44 Indels: 0
Query Match: 13 Gaps: 0
DB:

US-10-817-483-2 (1-239) x ADS62464 (1-720)

QY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 1 ATGGATCTGCGCTTAATTTCCGCTCCCACTTCACAGAAAGACCTCGACCCCGGAGCT 60
QY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTTCGCCAGCAGACTGGGCTTCCACTCTTTCGCTCGATTCGGGCTCCAAATGTTGCTCCAG 120
QY 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuValGlyThrThrArgLeuTyr 60
DB 121 CTGTCAACCGGAAGCGACGACCAACAGTGAAGAACTGAAGGAACGAGCGCTCATAC 180
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB 181 CTGTGATGATCGGCTCTGCTGTAAGGTTATCATCGACGCAAGCAAGCTCATGAAGGCTG 240
QY 81 IleaAgluValHisAsnHisGluAlaLysGlyGlyLeuIleLeuGluGlyGlySerIle 100
DB 241 ATGGGGAAGTGTATTAATTAATGAGGCCACGCGGGCTTATTCCTGAGGAGAGATCTATC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 301 TCGTTGCTCAAGTGCATGCGCAAGCAGTTATTGAGAGTGCAGATTTTCGTTGGCATATT 360
QY 121 IleaArgAngluLeuAlaAspGluIleLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 140
DB 361 ATTCGCCAGAGTTAGCAGACGAAAGACCTTCATGAACTGGCCAAAGCCAGATTAAAG 420
QY 141 GlnMetLeuArgProSerIleGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACGCCCTGCTGCAGGCCCTTCTATTATTCAGAAAGTTGGATTGTTGGAAA 480
QY 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 481 GAGCTTCGGCTCAGGCCCACTACTGAAAGATCGATGATATCGATATCCATGTTGTTT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB 541 GCTACCCAGAACCAAGATCCATCCGATATGCTATTGACAGCTTGACGACAGATATGGAGGAT 600

XX Recombinant DNA construct; transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KM bacterial polynucleotide; gene; ss.
XX Bacteria.
OS
XX
XX US2003233675-A1.
XX
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 38549; 122bp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 720 BP; 181 A; 166 C; 198 G; 175 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 1,11e-114 Length: 720
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 13 Gaps: 0

US-10-817-483-2 (1-239) x ADS62875 (1-720)

OY 1 MetaBleuAArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIleala 20

DB |||||
1 ATGATCTGCGCTTATTTTCGCTCAACTTCACAGGAACGTCGACCCGGAGCT 60
OY 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB CTGGCCAGCAGACTGGGCTTCCTCACTTCCTGCTGGATCGGGGTCCAAATGTTGCTCTG 120
OY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTy 60
DB CTGTCAACCGGAAGCGACGACCAACAGTGAAGAACTGAAGAAAGCAAGCGCTCTATAC 180
OY 61 LeuAspAspArgProLeuValLysGlyLleIleThrAlaLysGlnAlaHisGlnArgLeu 80
DB CTGTATGATCGGCTCTGATGAAGGTATCATCGACGACCAAGCAAGCTCATATAAGGCTG 240
OY 81 IleAlaGluValHisAsnHisGlnValAlaLysGlyGlyLeuLeuGluGlySerIle 100
DB ATGGGGGAGGTGTATATATATATGAGGCCACGCGGGCTTATTCCTGAGGAGGATCTATC 300
OY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTTPaenAlaAspPheArgTphsIle 120
DB TCGTTGCTCAAGTGCATGCGCAAGCAGTTATGAGATGCGGATTTTCGTTGCAATAT 360
OY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
DB ATTGCGCAGAGTTAGCAGACGAGAGACCTTCATGACGTGGCCAGGCCAGACTTAAG 420
OY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB CAGATGTTACGCCCTCGCTGAGGCTTCTATATATCAAGATGTTGATTTGGAA 480
OY 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB GAGCTCGGCTGAGGCGCCATCTGAAGAGATCGATGATATGCCATGTGTTT 540
OY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
DB GCTACCCAGAACCAATATCATCCGATATGCTATTCAGCTTGACGCAAGATATGAGAGAT 600
OY 201 LysLeuIleHisGlyTyrAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnLys 220
DB AAGTTGATTCATGGATGCTCTCAGAGATATCTCATCCATCGACGCCGACAAACAGAA 660
OY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
DB 661 TTCCCTCGAGTTAAAGCAGCGCTTACGACGAGATTCGAAGTCATTCGGAATG 717

RESULT 13
ADT62691
ID ADT62691 standard; DNA; 723 BP.
XX
XX ADT62691;
AC
XX 13-JAN-2005 (first entry)
DT
XX
XX
XX DNA encoding A. tumefaciens isopentenyl transferase (IPT) .
DE
XX
XX DNA plasmid; transfer DNA; T-DNA; Agrobacterium Ti plasmid; transgene;
KM expression cassette; transgenic plant; transgenic;
KM isopentenyl transferase; IPT; ds.
XX
XX
XX Agrobacterium tumefaciens.
OS
XX
XX
XX WO2004092390-A2.
XX
XX
XX 28-OCT-2004.
PD
XX
XX 09-APR-2004; 2004WO-US011000.
PF
XX
XX 09-APR-2003; 2003US-0461459P.
PR
XX
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
PA
XX

PI Gilbertson L, Krieger E, Zhang W, Ye X;
XX WPI; 2004-758349/74.
XX
XX New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid
PT first border region linked to a transgene linked to an Agrobacterium Ti
PT plasmid second border region, useful for enhancing production of
PT transgenic plants.
XX
XX Example 1; SEQ ID NO 2; 77bp; English.
XX
XX The present invention relates to a DNA plasmid comprising a transfer DNA
CC (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked
CC to at least one transgene linked to an Agrobacterium Ti plasmid second
CC border region, and located in the DNA plasmid outside of the T-DNA is a
CC plant expression cassette comprising a plant cell non-lethal negative
CC selectable marker gene linked to a vector backbone DNA. Also disclosed
CC are a method for enhancing the selection of transgenic plants that do not
CC contain vector backbone DNA, a method for reducing the copy number of a
CC transgene in a plant cell, and a transgenic plant produced by the method.
CC The DNA plasmid comprises the expression cassette comprising a promoter
CC that functions in plant cells operably linked to a plant cell non-lethal
CC negative selection marker gene. The promoter is a constitutive promoter.
CC The promoter expresses the linked non-lethal negative selection marker
CC gene product in tissue culture during plant regeneration. The plant cell
CC non-lethal negative selectable marker gene comprises a plant hormone
CC biosynthetic pathway gene, degradative gene, biosynthetic pathway
CC substrate-diverting gene or signaling gene, or metabolic interference
CC gene. The transgene is a plant positive selectable marker gene selected
CC from antibiotic resistance and herbicide resistance. The transgene
CC comprises a transgene of agronomic interest. The plant hormone
CC biosynthetic pathway gene is selected from gibberellin acid pathway
CC genes, cytokinin pathway genes, auxin pathway gene, ethylene pathway
CC genes, and abscisic acid pathway genes. The plasmid is useful for
CC enhancing the production of commercially viable transgenic plants. The
CC present sequence represents DNA encoding Agrobacterium tumefaciens
CC isopenentenyl transferase (IPT) enzyme. This sequence is used as a non-
CC lethal negative selectable marker.
XX
XX Sequence 723 BP; 183 A; 166 C; 198 G; 176 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. NO.: 1,12e-114 Length: 723
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 13 Gaps: 0

US-10-817-483-2 (1-239) x ADR62691 (1-723)

QY 1 MetaspLeuArgLeuIlePheGlyProThrcysThrglyLysThrSerThraIleAa 20
DB 1 ATGATCTGCGCTCTAATTTTCGGTCCACTTCGACAGAAAGACGTGACCGGGTACT 60
QY 21 LeuAlaGlnGlnThnglyLeuProValleuSerLeuAspArgValGlnCysCysProGln 40
DB 61 CTGGCCGACAGACAGCGGCTTCCTTCAGTCTTCGTCGATCGGTCCAATGTTGCTTAG 120
QY 41 LeuSerThnglySerGlyArgProThrcysValGlnGlyLeuLysGlyThrThraArgLeuTyr 60
DB 121 CTGTCAACCGGAGGAGGAGCAACACATGAGAGAACTGAAAGAACACCGCTTATAC 180
QY 61 LeuAspArgProLeuVallysglyIleIleThraIalysGlnAlaHisGlnArgLeu 80
DB 181 CTGTGATGCGGCTCTGGTGAAGGGTATCATCGACGCAAGCAAGCTCATGAAGGCTG 240
QY 81 IleAlaGlyValHisAsnHisGlnAlaIalysGlyIleuIleGlnGlySerIle 100
DB 241 ATGGGGAGGGTGTATATATATGAGGCCACGCGGGGCTTATTTTGAAGGAGATCTATC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120

DB 301 TCGTGTCTCAAGTCATGCGGCAAGACGATTATGAGTGGGATTTTCGTGCAATATT 360
QY 121 IleArgAsnGlyLeuAlaAspGlyGlnSerPheMetSerValAlaIleThrArgValIys 140
DB 361 ATTCGACACAGATTGACAGACGAGAGACCTTCATGTACGTCGACGACGACGAGTTAAG 420
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
DB 421 CAGATGTTACGCCCTGCTGACAGGCTTCTTATTTCCAAAGTTGGTGTATCTTTGAAA 480
QY 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuPhe 180
DB 481 GAGCTCGGCTGAGGACCATCTGAAAGATCATGATGATGATGATGATGATGATGATGAT 540
QY 181 AlaThrGlnGlnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGlnAsn 200
DB 541 GCTGCGCAGAACCCAGATCACATCCGATATGTATGACGCTTGACGAGATATGAGAGAT 600
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnIle 220
DB 601 AAGTTGATTCATGGGATTCCTCAGAGATATCTTCATGACGACCCGACAAAGAACAGAA 660
QY 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
DB 661 TTCCTCGAGTTACGACGCGCTTACAGACGATTCGAAAGTTCATTCATTCGAAATG 717

RESULT 14
ADR42934
ID ADR42934 standard; DNA; 723 BP.
XX
XX ADR42934;
AC
XX 18-NOV-2004 (first entry)
DT
XX IPT-like structural gene #1.
DE
XX
XX abscission zone; apical meristem; Plant Growth Regulant; Gene Therapy;
KW A6; abscission zone promoter; IPT; isopeny1 tranfese; ds.
XX
XX Unidentified.
OS
XX
XX WO2004074442-A2.
PN
XX
XX 02-SEP-2004.
PD
XX 13-FEB-2004; 2004WO-US004499.
PF
XX 14-FEB-2003; 2003US-0447833P.
PR
XX
XX (MONS) MONSANTO TECHNOLOGY LLC.
PA
XX
XX Bhat DG, Deng W, Eilers RJ, Nelson DE, Tennessee DJ;
PI WPI; 2004-635562/61.
DR
XX
XX New polynucleotides comprising a plant promoter that directs its
PT transcription into abscission zone(s), root, pod, wall, apical meristem,
PT or flower of plants, useful for producing a plant having increased yield
PT or agronomic trait.
XX
XX Claim 21; SEQ ID NO 16; 63bp; English.
PS
XX
XX The present invention relates to an isolated polynucleotide comprising a
CC plant promoter directing transcription of an operably linked
CC polynucleotide in at least one of the tissues selected from abscission
CC zone, root, pod, wall, apical meristem, and flower of plants. The
CC polynucleotides and methods are useful for producing a plant having
CC increased yield or a trait of agronomic interest when compared to a non-
CC transformed plant of the same genotype. The present sequence represents a
CC IPT-like structural gene. The sequence data for this patent is not
CC represented in the printed specification but was obtained in electronic
CC format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm.

Sequence 723 BP, 182 A, 166 C, 199 G, 176 T, 0 U, 0 Other:

Alignment Scores:

| Pred. No.: | 7,24e-114 | Length: | 723 |
|------------------------|-----------|---------------|-----|
| Score: | 1068.00 | Matches: | 205 |
| Percent Similarity: | 93.3% | Conservative: | 18 |
| Best Local Similarity: | 85.8% | Mismatches: | 16 |
| Query Match: | 86.8% | Indels: | 0 |
| DB: | 13 | Gaps: | 0 |

US-10-817-483-2 (1-239) x ADR42936 (1-723)

```

QY      1 MetAapLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB      1 ATGGATCTGCGCTTAATTTTCGGTCCAACTTCGACAGAAACGCGTCAAGCCGGTAGCT 60

QY      21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGln 40
DB      61 CTGGCCACGACAGCTGGGCTTCAGTCTCTTCGCTCGATCGGGGTCCAAATGTTGCTCTCAG 120

QY      41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB      121 CTGTCAACCGGAGAGGGAGGACCAACAGTGAAGAACTGAAGAAACGACCGCTCATATC 180

QY      61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB      181 CTTGATGATCGGCTCTGCTGAAGGGTATCATCGCAGCCAAACCAAGCTCATGAAGGCTG 240

QY      81 IleAlaGluValHisAsnHisGluValLysGlyLysGlyLeuIleLeuGlnGlyLysSerIle 100
DB      241 ATGGGGGGGGGTATATATATATAGAGGCCCAAGCGGGCTTATCTTGAGGAGAGATCTATC 300

QY      101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTTPAsnAlaAspPheArgTTPHisIle 120
DB      301 TCGTTGCTCAACTGCATGCGCAGCAAGCAAGTATTTGAGAGCCGATTTTCGTTGCCATAT 360

QY      121 IleArgAsnGluLeuAlaAspGlnGluSerPheMetSerValAlaLysThrArgValLys 140
DB      361 ATTCGCCACGAGTTGACAGACGAAAGACCTTCATGAAGTGGCCAAAGCCAGAGTTAAG 420

QY      141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTyrArg 160
DB      421 CAGATGTTACCGCCCTGCGACAGCCCTTTTATTTATTCAAAGATGGTATCTTTGGAAA 480

QY      161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB      481 GAGCCTCGGCTGAGGCCCATTAAGAAAGATCGATGATTCGATATCCCATGTTGTTT 540

QY      181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
DB      541 GCTACCCAGAACCAATCATCATCCATATGCTATTGAGCTTGACGCAAGATATGAGGAT 600

QY      201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnLys 220
DB      601 AAGTTGATTCATGGGATCGCTCAGAGATATCTCATTCATGCGCAGCAAAACAAAGGAAA 660

QY      221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
DB      661 TTCCCTCGAGTTAACGCAAGCCGCTTACGACGATTCGAAGTTCATCCATTCGGAATG 717

RESULT 15
ID      ADR42936 standard; DNA; 723 BP.
XX      ADR42936;
XX      18-NOV-2004 (first entry)
XX      IPT-like structural gene #2.
DE      IPT-like structural gene #2.
XX      abscission zone; apical meristem; Plant Growth Regulant; Gene Therapy;
XX      A6; abscission zone promoter; IPT; isopentenyl transfease; ds.

```

Unidentified.

WO2004074442-A2.
02-SEP-2004.
13-FEB-2004; 2004WO-US004499.
14-FEB-2003; 2003US-0447833P.

(MONS) MONSANTO TECHNOLOGY LLC.

Bhat DG, Deng M, Eilers RJ, Nelson DE, Temessen DJ;

WPI; 2004-635562/61.

New polynucleotides comprising a plant promoter that directs its transcription into abscission zone(s), root, pod, wall, apical meristem, or flower of plants, useful for producing a plant having increased yield or agronomic trait.

Claim 21; SEQ ID NO 18; 63pp; English.

The present invention relates to an isolated polynucleotide comprising a plant promoter directing transcription of an operably linked polynucleotide in at least one of the tissues selected from abscission zone, root, pod, wall, apical meristem, and flower of plants. The polynucleotides and methods are useful for producing a plant having increased yield or a trait of agronomic interest when compared to a non-transformed plant of the same genotype. The present sequence represents a IPT-like structural gene. The sequence data for this patent is not represented in the printed specification but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm.

Sequence 723 BP, 182 A, 166 C, 199 G, 176 T, 0 U, 0 Other:

Alignment Scores:

| Pred. No.: | 7,24e-114 | Length: | 723 |
|------------------------|-----------|---------------|-----|
| Score: | 1068.00 | Matches: | 205 |
| Percent Similarity: | 93.3% | Conservative: | 18 |
| Best Local Similarity: | 85.8% | Mismatches: | 16 |
| Query Match: | 86.8% | Indels: | 0 |
| DB: | 13 | Gaps: | 0 |

US-10-817-483-2 (1-239) x ADR42936 (1-723)

```

QY      1 MetAapLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB      1 ATGGATCTGCGCTTAATTTTCGGTCCAACTTCGACAGAAACGCGTCAAGCCGGTAGCT 60

QY      21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGln 40
DB      61 CTGGCCACGACAGCTGGGCTTCGATCTCTTCGCTCGATCGGGGTCCAAATGTTGCTCTCAG 120

QY      41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB      121 CTGTCAACCGGAGAGGGAGGACCAACAGTGAAGAACTGAAGAAACGACCGCTCATATC 180

QY      61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB      181 CTTGATGATCGGCTCTGCTGAAGGGTATCATCGCAGCCAAACCAAGCTCATGAAGGCTG 240

QY      81 IleAlaGluValHisAsnHisGluValLysGlyLysGlyLeuIleLeuGlnGlyLysSerIle 100
DB      241 ATGGGGGGGGGTATATATATATAGAGGCCCAAGCGGGCTTATCTTGAGGAGAGATCTATC 300

QY      101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTTPAsnAlaAspPheArgTTPHisIle 120
DB      301 TCGTTGCTCAAGTGCATGCGCAGCAAGCAAGTATTTGAGATGCGGATTTTCGTTGCCATAT 360

QY      121 IleArgAsnGluLeuAlaAspGlnGluSerPheMetSerValAlaLysThrArgValLys 140
DB      361 ATTCGCCACGAGTTGACAGACGAAAGACCTTCATGAAGTGGCCAAAGCCAGAGTTAAG 420

```

| | | | |
|----|-----|---|-----|
| Qy | 141 | GlnMetLeuAxpProSeAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTPaG | 160 |
| | | | |
| Db | 421 | CAGATGTTACGCCCTGCTGCAGAGCCTTTCTATTATTCAGAGTGGTATTCATTGGAAA | 480 |
| Qy | 161 | GluProArgLeuAxpProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe | 180 |
| | | | |
| Db | 481 | GAGCCTCGCGTCGAGGCCCATCTACTGAAAGAAATCGATTCGAAATATCCAGTGGTTT | 540 |
| Qy | 181 | AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn | 200 |
| | | | |
| Db | 541 | GCTAGCCGAGACCAATCATCATCCGATATAGTCATTCGACCTTGACCCAGATATGAGAGAT | 600 |
| Qy | 201 | LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnIlys | 220 |
| | | | |
| Db | 601 | AAGTTGATTCAGAGGATCGCTCAGAGGATTCATCATCAACGACGCGAACAAGAACGAAA | 660 |
| Qy | 221 | PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyIProProPheArgMet | 239 |
| | | | |
| Db | 661 | TTCCTTCGAGTTAACGCACCGCTTACAGACGATTCGAAGGTATCATCTTCGGAATG | 717 |

Search completed: June 26, 2006, 19:53:26
Job time : 655 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2006, 19:46:01 ; Search time 4446 Seconds
(without alignments)
4509.015 Million cell updates/sec

Title: US-10-817-483-2

Sequence: 1 MDLRIFFGPTCTGKTSTAIA.....KPLVGAATVAFAFSPPRM 239

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

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-OUTPMT=PCT -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs803p
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_eest3:*
3: gb_eest4:*
4: gb_eest5:*
5: gb_eest6:*
6: gb_hic:*
7: gb_eest2:*
8: gb_eest7:*
9: gb_eest8:*
10: gb_eest9:*
11: gb_ges81:*
12: gb_ges82:*
13: gb_ges83:*
14: gb_ges84:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 124 | 10.1 | 883 | 14 | DU740683 |
| 2 | 115 | 9.3 | 763 | 5 | CK714752 LECAD01B1 |
| 3 | 112.5 | 9.1 | 692 | 3 | BO972287 OHC307 Y |
| 4 | 112 | 9.1 | 656 | 8 | CV005106 pam01-11m |

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| 5 | 111.5 | 9.1 | 886 | 10 | DT209523 | DT209523 JGI CAAS1 |
| 6 | 109.5 | 8.9 | 867 | 10 | DT280070 | DT280070 JGI_CAAV9 |
| 7 | 107 | 8.7 | 1769 | 6 | AK166259 | AK166259 Mus muscu |
| 8 | 106.5 | 8.7 | 831 | 12 | CC391172 | CC391172 PUCY57TD |
| 9 | 106.5 | 8.7 | 916 | 12 | CC391169 | CC391169 PUCY57TB |
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| 16 | 102 | 8.3 | 1951 | 6 | AK010176 | AK010176 Mus muscu |
| 17 | 102 | 8.3 | 2061 | 6 | AK003556 | AK003556 Mus muscu |
| 18 | 101.5 | 8.3 | 756 | 10 | DT151607 | DT151607 JGI_ANNO3 |
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| 20 | 101 | 8.2 | 2734 | 6 | AK154256 | AK154256 Mus muscu |
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| 26 | 98.5 | 8.0 | 741 | 4 | BX733862 | BX733862 BX733862 |
| 27 | 98.5 | 8.0 | 833 | 9 | CK425315 | CK425315 JGI_XZG12 |
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| 36 | 98.5 | 8.0 | 1442 | 10 | DT970650 | DT970650 CLJ129-G0 |
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| 38 | 98 | 8.0 | 675 | 2 | BG973165 | BG973165 602842454 |
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| 42 | 97 | 7.9 | 1074 | 10 | DM664632 | DM664632 CNB326-G0 |
| 43 | 97 | 7.9 | 1738 | 6 | AK150081 | AK150081 Mus muscu |
| 44 | 97 | 7.9 | 1751 | 6 | AK152329 | AK152329 Mus muscu |
| 45 | 97 | 7.9 | 1768 | 6 | AK088824 | AK088824 Mus muscu |

ALIGNMENTS

| RESULT 1 | LOCUS | DEFINITION | ACCESSION | VERSION | KEYWORDS | SOURCE | ORGANISM | REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT |
|----------|-------------------------------|---|-------------------------------|---------|---|---|---|--|---|--|-------------------------|---|
| DU740683 | APK1584.g2 | HF70_10-07-02 uncultured marine microorganism | DU740683 | 1 | GI:85750517 | uncultured marine microorganism HF70_10-07-02 | uncultured marine microorganism HF70_10-07-02 | 1 (bases 1 to 883) | DeLong, E. F., Preston, C. M., Mincer, T., Rich, V., Hallam, S. J., Frigaard, N. U., Martinez, A., Sullivan, M., Edwards, R., Chisholm, S. W. and Karl, D. M. | Comparative genomics reveals ecological trends in stratified microbial communities in the ocean's interior | Science (2006) In Press | Contact: Susan Lucas, Alex Copeland, Sam Picluck, Alla Lapidus, Kerrie Barry, Trijana Glavinadeliro, David Bruce, Paul Richardson and Edward Delong |
| DU740683 | US DOE Joint Genome Institute | US DOE Joint Genome Institute | US DOE Joint Genome Institute | 2800 | Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA | Tel: 617-253-5271 | Fax: 617-253-2679 | Email: pmlrichardson@lbl.gov; delong@mit.edu | Sample Date: 10/7/2002 | Coordinates: 22.45 N, 158 W | Depth 70 m | |

Qy 109 SerArgTYrTPsAnlaAspPheArgTrpHisIleIleArgAsnGluLeuAlaAspGlu 128
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Db 580 GAG-----AGATCTTAGATGACTGCAGAA 606
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Qy 149 LeuSerIleIleGlnGluLeuValGlnLeu-----TPrArg----- 160
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Db 607 GGAAGTAAAGTGAAGAGCTTATAGATTGTTGATGAGAGAAAGTTGCAGAGAAACA 666
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667 GCTCTTTGCGTCAAGTAACTGAACCTGTGTTCCGTCGCTTGAAGGT 717
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LOCUS QHC3b07.y9.ab1 OH ABCDI sunflower RHA801 Helianthus annuus cDNA
DEFINITION clone QHC3b07, mRNA sequence.
BO972287
ACCESSION BO972287.1 GI:22389810
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Helianthus annuus (common sunflower)
Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
1 (bases 1 to 692)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmndson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
singleton, see http://cgdb.ucdavis.edu/ for details.
Plate: QHC3 row: b column: 07.
Location/Qualifiers
1. 692
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/mol_type="mRNA"
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/db_xref="taxon:4232"
/clone="QHC3b07"
/lab_host="E.coli"
/clone_id="OH ABCDI sunflower RHA801"
/note="Vector: pBRCDNA5f1ab; The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_TISSUE=hu11s
TAG_LIB=OH ABCDI sunflower RHA801
TAG_SEQ=GTAGTCGGG"
ORIGIN
Alignment Scores: 0.0481 Length: 692
Pred. No.:

Score: 112.50 Matches: 49
Percent Similarity: 42.1% Conservative: 36
Best Local Similarity: 24.3% Mismatches: 94
Query Match: 9.1% Indels: 23
DB: 3 Gaps: 6
US-10-817-483-2 (1-239) x BO972287 (1-692)
Qy 5 LeuIlePheGlyProThrCysThrGlyIylsThrSerThrAlaIleAlaGlnGln 24
|||||
Db 86 CTATTCGTAAGTAGAGAGAAACCGTAAACCGACACTGATGCTATAGCCGAGAG 145
|||||
Qy 25 ThrGlyLeuProValLeuSerIleuAspArgValGlnCysCysProGlnLeuSerThrGly 44
|||||
Db 146 GCGAAGGTCCCGGTGTTGAGGTTAAAGCTCAACGTTTAGAGCGCGGCTTAGGGTGGGC 205
|||||
Qy 45 SerGlyArgProThrValGlnGluLeuIylsGlyThrThrArg----- 58
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Db 206 CAGAGTCATCCACAGCTTAGAGAACTGTTCCAAACGCCAGATCTGCGCCTGTATC 265
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Qy 59 LeuTYrLeuAspAspArgProLeuValIylsGly-----IleIleThrAla 73
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|||||
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Qy 185 GlnIle 186
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Db 677 GAACCT 682
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DEFINITION pam01-11ms3-a09 Pam01 Persea americana cDNA clone pam01-11ms3-a09
5', mRNA sequence.
CVO05106
ACCESSION CVO05106.1 GI:51364329
VERSION
KEYWORDS
SOURCE
ORGANISM
Persea americana (avocado)
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Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
Persea.
1 (bases 1 to 656)
dePamphilis,C., Carlson,J., Ma,H., Solis,D., Solis,P.,
Opdenheimer,D., Frohlich,M., Doyle,J., Tanksley,S., Webb,M.,
Leebens-Mack,J., Landherr,L., Ilut,D. and Wall,K.
Generation of ESTs from early flower buds of Persea americana
Unpublished (2003)
Contact: Claude dePamphilis or James Leebens-Mack
Mueller Laboratory

| | | | | |
|------------|--|---|--|-----|
| OY | | 33 | AAPAGVAlGInCyScySPProInleusearThrglyserGIYAArgPProThrValGlUnlu | 52 |
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| Db | | 382 | GCTGACCTGCAGTACGAGATATGAGAGATGACATGACAAGACCGCTTA----- | 429 |
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| Db | | 526 | AACGAC-----CGATGTGGGGAGAGCCCAATACAGAAAAGTAAATC | 564 |
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| Db | | 565 | CACGGGGTTATCACTCCTTT---CTTATGTGTAACAATACAGAAAAAGTTTCCTTA | 621 |
| OY | | 224 | ValGIAlaThrAlaValaGIUAlaPheGIUGIPro | 235 |
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| | | males and females pooled (H) Pimphales promelas cDNA clone | | |
| VERSION | | CAVAV9004.5', mRNA sequence. | | |
| KEYWORDS | | DT280070 DT280070.1 GI:73582019 | | |
| SOURCE | | EST. | | |
| ORGANISM | | Pimphales promelas | | |
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| | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| | | Actinopterygii; Neopterygii; Teleostei; Osteichthyes; | | |
| | | Cypriniformes; Cyprinidae; Pimephales. | | |
| | | 1 (bases 1 to 867) | | |
| | | Richardson,P., Lucas,S., Rokhar,D., Deter,J.C., Ng,D.C., | | |
| | | Brockstein,P. and Lindquist,E.A. | | |
| | | DOE Joint Genome Institute Pimphales promelas EST project | | |
| | | Unpublished (2005) | | |
| TITLE | | Other_ESTs: JGI_CAAV9004.rev | | |
| REFERENCE | | Contact: Lindquist,E.A., Richardson,P. | | |
| AUTHORS | | DOE Joint Genome Institute | | |
| | | 2800 Mitchell Drive, Walnut Creek, CA 94598, USA | | |
| | | Tel.: 925 296 5600 | | |
| | | Fax: 925 296 5710 | | |
| | | Email: cdna@jgi-psf.org | | |
| JOURNAL | | cDNA library Preparation: DOE Joint Genome Institute: | | |
| COMMENT | | http://www.jgi.doe.gov | | |

DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
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 High quality sequence stop: 782.
 Location/Qualifiers
 1. 867
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 /db_xref="taxon:90988"
 /clone="CAAV9004"
 /cruise_type="testis"
 /clone_lib="CAAV Pimephales promelas testis 7-8 month adults, males and females pooled (h)"
 /note="Vector: pCMVSPORT6; The library was made from dt primed cDNA and cloned into Invitrogen vector pCMVSPORT6. Poly A RNA were primed with an oligo dt primer (5'-GACTAGTCTGATCGAGCGCGCCCTTTTCTTTT-3') ligated to a SalI adapter (5'-TCGACACGCGTCG and 5'-CGGACGCGTCGG) and digested with NotI. cDNA was size selected using 1.1% agarose gel electrophoresis (L ~0.5-1.2k, M ~1.2-2.5k, H ~2.5k) then ligated into NotI and SalI digested pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute."

ORIGIN
 Alignment Scores:
 Pred. No.: 0.148 Length: 867
 Score: 109.50 Matches: 52
 Percent Similarity: 42.0% Conservative: 37
 Best Local Similarity: 24.5% Mismatches: 76
 Query Match: 8.9% Indels: 47
 DB: 10 Gaps: 13

US-10-817-483-2 (1-239) x DT280070 (1-867)

| | | | |
|----|-----|--|--------------------------|
| OY | 33 | AsparValaIgcIncyScyPspGlnInuSerThrglySerGlyArgProThrValaIgcInu | 52 |
| DB | 293 | GACGCGTCTCGACATATAGCGCGTGTGTGCGATATCCGAGCCCGTATGGGGAAG | 352 |
| OY | 53 | LeuIysGlyThrThrArgLeuTyIleuAsp---- | ArgProIeuValIysGlyIle 70 |
| DB | 353 | CTGTACACCGAGACCAAGGTGTTTCTGAGAACCAACGTCGCCGACCTGTTCAAGAGATC | 412 |
| OY | 71 | IleThrAlaIysGlnAlaHisGluArgLeuIleAlaGluValHisAsnHis----- | 87 |
| OY | 413 | CTG-----GAGCTGAAGAGAAAGGTTTGTGATGTATCAAGATACGGGAGAG | 463 |
| OY | 88 | GluAlaIysGlyGluIleuIleuGluGlySerIleSerLeuIeuArgCysMetAla 107 | |
| DB | 464 | TACACCAAGGTCGAGTACATGAT-----TGCCTA-- | 496 |
| OY | 108 | GlnSerArgTyIrrPasnAlaAspPheArgTrpHisIleIleArgAsnGluIeuAlaAsp | 127 |
| DB | 497 | ---TACAGATACCTGAACACACAGATTC-----ATTAGAAGAACAGCTGACCGAA | 544 |
| OY | 128 | GluGluSerPheMetSerValAlaIysThrArgValIysGlnMetLeuArgProSerAla | 147 |
| DB | 545 | GCTGACCTGCAGTACGGAATATGAGAGATGACATGAACGAGCCGTTA----- | 592 |
| OY | 148 | GlyIeuSerIleIleGlnGluIeuValGlnIeuTrpArg-----GluProArg | 163 |
| DB | 593 | ---ATGGAGATCGGAGAGCTTGCAATGACACATGTGGGAACTTAATGATTAAGCT--- | 646 |
| OY | 164 | LeuArgProIleIeuGluGlyIleAspGlyTyArgTyAlaIleuIlePheAlaThrGln | 183 |
| DB | 647 | CTTCAACCAATGCTCATGCGGATG-----CTTCTGAAGAAGATCAAG | 688 |
| OY | 184 | AsnGlnIleThrProAspMetLeuIeuGlnIeuAspMetGluAsnIysLeuIle | 203 |
| DB | 689 | AACGAC-----CGAATGTGGGAGAGCCCAATCAGAAATGAATGAATAC | 727 |

[illegible]

REFERENCE
AUTHORS
 5 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nishida, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schmitt, L.M., Kanapin, A., Matsuda, H., Barlow, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousine, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazier, K.S., Gassteland, T., Glatfeld, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Guticinski, S., Hirokawa, N., Jackson, J.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lehman, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, M.J., Petrea, G., Peocle, G., Petrovsky, N., Pillai, R., Pontus, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, J., Reid, J., Ring, B.Z., Ringwald, M., Sanderlin, A., Schneider, C., Sempke, C.A., Setou, M., Shmad, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Wanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carinci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Aikawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
CONSRMT
TITLE
 PANTOM Consortium
 Analyses of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 421 (6915), 563-573 (2002)
 12466851
JOURNAL
PUBMED
REFERENCE
AUTHORS
 6 Carinci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Meada, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V.B., Bremner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aldins, V., Allen, J.E., Ameseli, Impombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Banasi, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Chiu, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Engolinn, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gusticinski, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Isikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kasasawa, Y., Kelson, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Lin, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabbar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, M.J., Pavesi, G., Peocle, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z., Ringwald, M., Roest, B., Ruan, Y., Salzberg, S.L., Sanderlin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Sempke, C.A., Seno, S., Seese, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugiyara, K., Sultana, R., Takanaka, Y., Takt, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamashita, H., Zdobych, R., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T., Brusic, V., Quackenbush, J., Wahlestedt, C., Matic, K.A., Seno, S., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori, Katayama, M., Suzuki, M., Aoki, J., Aikawa, T., Iida, J., Imanura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Kono, H., Nakano, K., Nimmiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Watahiki, A., Okamura-Ono, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
CONSRMT
TITLE
 The transcriptional landscape of the mammalian genome
 PANTOM Consortium

JOURNAL Science 309 (5740), 1559-1563 (2005)
PUBMED 16141072
REFERENCE 7
AUTHORS Kacanya,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M., Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H., Carninci,P., Hayashizaki,Y., Wells,C., Fritch,M., Ravaai,T., Pang,K.C., Hallinan,J., Matick,J., Hume,D.A., Lipovich,L., Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A., Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and Wahlstedt,C.
CONSRM RIKEN Genome Exploration Research Group
TITLE Antisense transcription in the mammalian transcriptome
JOURNAL Science 309 (5740), 1564-1566 (2005)
PUBMED 16141073
REFERENCE 8 (bases 1 to 1769)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S., Kawai,K., Kojima,M., Kono,H., Murata,M., Nakamura,M., Ninomiya,N., Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watabiki,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
FEATURES
source location/Qualifiers
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AAGFKCVLPHDVAVLTDKLPYVAMOKYFASGCTYSDSIFLSVAMQIMKEI
PRITOLDLKKTKNIRLFEEDFDFLGAIVGIREMQPYRHTFNFQPHRENTKRV
GDPPREGLPGRNSGVMLNLEMRQSPYSHLEPAWQQLDKYHFGHGLGDQDFPT
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ORIGIN

Alignment Scores: 0.804 1769
Pred. No.: 107.00 Matches: 49
Score: 40.2% Conservative: 31
Percent Similarity: 24.6% Mismatches: 65
Best Local Similarity: 8.7% Indels: 54
Query Match: 6 Gaps: 11
DB:

US-10-817-483-2 (1-239) x AKI66259 (1-1769)
QY 39 ProGlnLeuSerThrGlySerGlyArgProThr-----ValGlnGlnLeuLys 54
Db 258 CCCGAGCTGGCGCCGGGGGCTCCGGCGCGGCTCCGGGCGCAAGGCCAAGAGCTGGAG 317
QY 55 GlnThrThrArgLeuTyrLeuAspAspArgProLeuValLysGlyTleIleThrAlaLys 74
Db 318 GGC-----GGCGTGTGTGTCCCGGTG 338
QY 75 GlnAlaHISGlnArgLeuIleAlaGluValHisAsnHis-----GlnAlaLys 90
Db 339 GACTGCCACGACCTGATGATGTTCCCAAGCGGAGCAGAGCCGCCGCTGACGCGCAAG 398
QY 91 GlyGlyLeuIleLeuGlnGlyGlySerIleSerLeuLeuArgCysMetAlaGlnSerArg 110
Db 399 GCTGGGTGGCGGCTGAGC-----TCCCTGTGCGGCTC-----431
QY 111 TyrTrpAsnAlaAspPheArgTrpHisIleIleArgAsn---GlnLeuAlaAspGlnGlu 129
Db 432 -----GCCAAGCTTGAGCGCAGCAGAGGCTTAACCTTCACCTTCGTGTGAGCGAAG 482
QY 130 SerPheMetSerValAlaIleThrArgValLysGlnMetLeuArgProSerAlaGlyLeu 149
Db 483 GCCACCGCGGAGGTGGCCAAAGCCCTGCTGGGAGGCTCTCCGCCCGCGGCTTC 542
QY 150 Ser-----IleIleGlnGlnLeuValGlnLeuTrpArgGluProArgLeuArgPro 166
Db 543 AAGTGCAGAGCATCTTCCAGATGATGTGCTGTGCTG-----ACAGATAGCTCTTCC 596
QY 167 IleLeuGlnGlyIleAspGlyTyrArgTyrAla-----177
Db 597 GTCTGGAGCGCATCTTCCAGATGATGTGCTGTGCTGCGGAGCTACACGACATCC 656
QY 178 -----LeuLeuPheAlaThrGlnAsnGlnIleThrPro-----AspMetLeuLeu 192
Db 657 ATCTTCTTCTCTCTCCGTTGCCATGCACGATCATCCCAAGATGCCGAGATCATC 716
QY 193 GlnLeuAspAlaAspMetGlnAsnLysLeu---IleHisGlyIleAlaGlnGluPhe 210
Db 717 CAGCTGGAACCTTGACCTGAAGATATAGAACCAACATCCGAGAGCTTTTGAGAGAGTTT 773
RESULT 8
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LOCUS PNHCV57TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa423117,
DEFINITION genomic survey sequence.
ACCESSION CC3911172
VERSION CC3911172.1 GI:30871262
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 831)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uteback,T.,
Benner,J.A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennett,J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PNHCV57TB
Contact: Cathy WhiteLaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteLaw@tigr.org
Seq primer: TP
Class: sheared ends.
Location/Qualifiers
1..831
/organism="Zea mays"

Db 850 AGGTCCCTTGTGATTTGGCGCTTGCGCCGTGCGATTGAGAAAGTTTGG 897

RESULT 10
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DEFINITION CGA123-E10.y1d-s SHGC-CGX2 Gasterosteus aculeatus cDNA clone
ACCESSION DMS96236
VERSION DMS96236.1 GI:85172170
KEYWORDS EST.
SOURCE Gasterosteus aculeatus (three spined stickleback)
ORGANISM Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.
1 (bases 1 to 1113)
REFERENCE Kingsley,D.M., Peichel,C., Knecht,A., Balabhadr,a,S., Grimwood,J.,
AUTHORS Dickson,M., Schmutz,J. and Myers,R.M.
TITLE Expressed sequence tags from Gasterosteus aculeatus (2004)
JOURNAL Unpublished (2004)
COMMENT Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@hgc.stanford.edu
Plate: 123
High quality sequence Etop: 889.
Location/Qualifiers
1..1113
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/strain="Conner Creek sticklebacks, WA USA"
/db_xref="taxon:69293"
/clone="CGA123-E10"
/sex="mixed male and female"
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/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CGX2"
/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTGATTCGATCGAGCGCGCGCC(7)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna_library_construction_fa9.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria."

ORIGIN

Alignment Scores:

| Pred. No.: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|------------|--------|---------------------|------------------------|--------------|---------|----------|---------------|-------------|---------|-------|
| 0.612 | 105.50 | 41.5% | 22.7% | 8.6% | 1113 | 47 | 39 | 84 | 37 | 11 |

US-10-817-483-2 (1-239) x DMS96236 (1-1113)

QY 33 AsparagVAlGInCySProGInLeuserThrGlySerGlyArgProThrValGluGlu 52
Db 197 GACCGCTTCTCCGACATTATGCTTGTGCGTTCGATCCAGACGCTTTGGGGAGAG 256
QY 53 LeuYsgLYThrThrArgLeuTYrLeuAspA-----ArgProLeuValYsgLYle 70
Db 257 TTATACAGAGAGACCAAGCTCTTTCTTGAATCATGTTCGCACTTATACAGAAAGTC 316
QY 71 lIethrAlaYsglAlaHIsGluArgLeuileAlaGluValHIsAsnHIs-----Glu 88
Db 317 CTA-----GAATCAGAGAAAGAAAGTTTATGATGTATACACAGATACCGGACGAG 367
QY 89 AlalYsgLYgLYleuileuGluGluGlySerIleSerLeuLeuArgCyeHecAlaGln 108
Db 368 TACAGCAGAGGA-----GCTGACTCATGAGACTGCTG----- 400
QY 109 SerArgTYrTPAsnAlaAspPheArgThrPHisIleIleArgAsnGluLeuAlaSpGlu 128
Db 401 TACAGGATTCACACACTCAGTTC-----ATCAGAGAGACAACTACAGAGACA 451
QY 129 GluserPheMetSerValAlaYsThrArgValYsglMetLeuArgProSerAlaGly 148
Db 452 GACCTGCAGTACGGCTACGATGGGGGTGACATGAACGAGCCGCTC----- 496
QY 149 LeuserIleIleGlnGluLeuValGlnLeuTPArgGluProArgLeuArgProIleLeu 168
Db 497 ATGAGATCGAGAGAGCTGGCCCTCGACATGTGGAGAGAACTAATGATGAGCCCTTCAG 556
QY 169 GluGlyIleAspGlyTYrArgTYrAlaLeuLeuPheAlaThrGlnAsnGlnIleThrPro 188
Db 557 GAT-----GTCCTGATCCGAGATGCTGTAATGAATCAAAAT 595
QY 189 AspMetLeuGlnLeuAspAlaAspMetGluAsnYsLeuIleHIsGlyIleAlaGln 208
Db 596 GAC-----CGTTGGGAGAGAACCTTAACAGAGAGATCATCAGGGGCTATCAAC 646
QY 209 GluPheLeuIleHIsAlaArgArgGlnGlnGlnIleYsPheProLeuValGlyAlaThrAla 228
Db 647 TCCTTT---GTTCAGTGTGAACAGTACAGAAAGATTTCACATC-----AAGTTTAT 697
QY 229 ValGluAlaPheGluGlyPro 235
Db 698 CAGGAATCTTCGAAAGGACCA 718

RESULT 11
LOCUS DT179124 876 bp mRNA linear EST 16-AUG-2005
DEFINITION JGI_ANNO47121.fwd ANNO Pimephales promelas whole (M) Pimephales
ACCESSION DT179124
VERSION DT179124.1 GI:73439175
KEYWORDS EST.
SOURCE Pimephales promelas
ORGANISM Pimephales promelas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Pimephales.
1 (bases 1 to 876)
REFERENCE Richardson,P., Lucas,S., Rokhear,D., Deter,J.C., Ng,D.C.,
AUTHORS Brokstein,P. and Lindquist,E.A.
TITLE DOE Joint Genome Institute Pimephales promelas EST project
JOURNAL Unpublished (2005)
COMMENT Other ESTs: JGI_ANNO47121.rev
DOE Joint Genome Institute
Contact: Lindquist,E.A., Richardson,P.
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
CDNA library Preparation: DOE Joint Genome Institute:
<http://www.jgi.doe.gov>
DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
Naming Conventions: EST name is generated by the concatenation of

QY 141 GlnMetLeuArgPro-----SerAlaGlyLeuSerIleIleGlnIleuVal 156
 Db 373 AAAGCTTTGACACAGGCTTCTATTGTGTCACAGGCTCAAGATGACAACTGAGCTGTGA 314
 QY 157 Gln----- 157
 Db 313 CAGAGATGCCAAGCTGTCAATTCACCGGAAGCATCCACACACAGCTCAGCTCGTG 254
 QY 158 -----LeuTPArgGluProArgLeuArgProIle 167
 Db 253 CAGCTCAGTCCCTGTGATGAGCTTTGCGAGTTTGGGGATTGATATTTTGGGACCATTC 194
 QY 168 LeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPheAlaThrGlnAsnGlnIleThr 187
 Db 193 CCAAGGCTGTGGTGGCTATGAGTAC-----CTATATGTGCCATTAAACAAGTTCACC 140
 QY 188 ProAspMet-----LeuLeuGlnLeuAspAlaAspMetGluAsnLysLeuIle 203
 Db 139 AAATGGCTGGAAAGCTCTTTCATCATCAAGATTGATTAATAATTCCCTCCATAGTTCCCTT 80
 QY 204 HisGlyIleAlaGlnLupPheLeuIleHisAlaArg 215
 Db 79 CGGGGATTGTCTCATTTGGGGTTCGAACACA 44
 RESULT 13
 CV857774 871 bp mRNA linear EST 30-NOV-2005
 LOCUS gonad.EST05250 Embryonic gonad cDNA library Gallus gallus cDNA 5',
 DEFINITION mRNA sequence.
 ACCESSION CV857774
 VERSION CV857774.1 GI:82786158
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 871)
 Shin,J.H., Kim,H., Lim,D., Jeon,M., Han,B.K., Park,T.S., Kim,J.K.,
 Lillehoj,H.S., Cho,B.W. and Han,J.Y.
 Analysis of chicken embryonic gonad expressed sequenced tags
 J. Anim. Genet. 37 (1), 85-86 (2006)
 CONTACT: Jae Yong Han, Ph. D.
 Division of Animal Genetic Engineering
 School of Agricultural Biotechnology, Seoul National University
 San 56-1, Silim-dong, Gwanak-gu, Seoul, 151-742, Korea
 Tel: +822-880-4810
 Fax: +822-880-4811
 Email: Jaehan@snu.ac.kr
 Seq primer: 73.
 FEATURES
 source Location/Qualifiers
 1..871
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 EcoRI; The libraries were synthesized using the
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 prepared, size-fractionated and inserted into the Uni-ZAP
 XR vector using XhoI linker-primer and EcoRI adaptor.
 After in vivo excision with E. coli strain SOLR, cDNA
 libraries from each contain each insert size range of
 0.5-3kb (n=20), and 0.5-5.5kb (n=20)."
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 Pred. No.: 102.50 Matches: 55
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Percent Similarity: 39.6% Conservative: 36
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 QY 42 SerThrGlySerGlyArgProThrValGlnIleu-----LysGly 55
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 CAV2005 5', mRNA sequence.
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 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Pimephales.
 1 (bases 1 to 881)
 Richardson,P., Lucas,S., Rokhsar,D., Dettler,J.C., Ng,D.C.,
 Brokstein,P. and Lindquist,E.A.
 DOE Joint Genome Institute Pimephales promelas EST project
 TITLE

JOURNAL COMMENT

Unpublished (2005)
Other_ESTS: JGI_CAAV2005.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
CDNA library preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone id and the direction of sequencing. The suffix 'fwd', indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
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Location/Qualifiers
1. 881

FEATURES source

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ORIGIN

Alignment Scores:

Pred. No.: 0.966 Length: 881
Score: 102.50 Matches: 51
Percent Similarity: 38.4% Conservative: 27
Best Local Similarity: 25.1% Mismatches: 72
Query Match: 8.3% Indels: 53
DB: 10 Gaps: 10

US-10-817-483-2 (1-239) x DT627881 (1-881)

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CK603491

LOCUS CK603491 818 bp mRNA linear EST 22-JAN-2004
DEFINITION AGENCOURT 17897721 NIH MGC 234 Rattus norvegicus cDNA clone
IMAGE:7193158 5', mRNA sequence.

ACCESSION

CK603491

CK603491.1 GI:41116810

KEYWORDS

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LRAM15054 row: p column: 20
High quality sequence stop: 622.
Location/Qualifiers
1. 818

FEATURES source

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/note="Organ: heart; Vector: pExpress-1; Site 1: SCORV; Site 2: NotI; RNA obtained from pooled heart tissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (TRI-reagent method). CDNA was primed using oligo-dT primer:
5'-pGACTAGTTCAGATCGGAGCGGCCGCCCTC(T)25-3' and cloned into the SCORV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.2 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_233) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus.p2n model

Run on: June 26, 2006, 19:47:30 ; Search time 187 Seconds
(without alignments)
3587.126 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Patent No. 6992237
; GENERAL INFORMATION:
; APPLICANT: Zinselmeyer, Chris
; APPLICANT: Haben, Jeff
; TITLE OF INVENTION: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/09/545,334B
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
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; SOFTWARE: FastSeq for Windows Version 3.0
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; OTHER INFORMATION: and General Genetics 216:388-394 (1989): terminator
; OTHER INFORMATION: from Zea mays, Gendank Accession #S78780.
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; Patent No. 6992237
; GENERAL INFORMATION:
; APPLICANT: Zinselmeier, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/09/545,334B
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
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; OTHER INFORMATION: Promoter from Zea mays, U.S. patent application 09/377,648;
; OTHER INFORMATION: Gene from Agrobacterium tumefaciens, Molecular and General
; OTHER INFORMATION: Genetics 216:388-394 (1989); terminator from Solanum
US-09-545-334B-9
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Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
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Qy 221 PheProleuValGlyAlaThraAlaValGluAlaPheGluGlyProProPheArgMet 239
Db 2185 TTCCCTTTGGTGGGCGCAGACAGCTGTGCAAGCGTTTGAAGGACCACTTTGCAATG 2241
RESULT 3
US-09-545-334B-12
; Sequence 12, Application US/09545334B
; Patent No. 6992237
; GENERAL INFORMATION:
; APPLICANT: Zinselmeier, Chris
```


APPLICANT: Haben, Jeff
APPLICANT: Tomes, Dwight
TITLE OF INVENTION: Regulated Expression of Genes in Plant
TITLE OF INVENTION: Seeds
FILE REFERENCE: 0803
CURRENT APPLICATION NUMBER: US/09/545,334B
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/129,844
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 3017
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter from Zea mays, Genbank Accession #U22344;
OTHER INFORMATION: Gene from Agrobacterium tumefaciens, Molecular and
OTHER INFORMATION: General Genetics 216:388-394 (1989); terminator from
US-09-545-334B-12

Alignment Scores:

| Pred. No.: | 1,3e-138 | Length: | 3017 |
|------------------------|----------|---------------|------|
| Score: | 1230.00 | Matches: | 239 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |
| Query Match: | 100.0% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-10-817-483-2 (1-239) x US-09-545-334B-12 (1-3017)

Qy 1 MetAapLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleala 20
Db 1408 ATGATCTACGCTAATTTTCGTCCTCACTGACAGAAAGACATCGACTCGATAGCT 1467
Qy 21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGln 40
Db 1468 CTGGCCAGCAGACAGCTGGCTCCAGTCTCTCGTCGATCGGCTCAATGCTGCTCTCA 1527
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyYThrThrArgLeuYr 60
Db 1528 CTATCAACCGGAAAGGGGGGAGCAACAGTGAAGAACTGAAGAAAGCACTGCTGTAC 1587
Qy 61 LeuAspAspArgProLeuValIysGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu 80
Db 1588 CTGTGATCGCCCTTTGGTAAAGGATCATTTACAGCAACAGCTCATGACGGCTC 1647
Qy 81 IleAlaGlnValHisAsnHisGlnAlaLysGlyLysLeuIleLeuGlnGlySerIle 100
Db 1648 ATTTGGAGGTGCACAAATCACAGAGCCAAAGCGGGCTTATCTTGAGGAGGATCTATC 1707
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgYrTrpAsnAlaAspPheArgTrpHisIle 120
Db 1708 TCGTTGCTCAGGTGATGGCCGAAGTCTTATTGGAACGGCGATTTTCGTGGCATATT 1767
Qy 121 IleArgAsnGlnLeuAlaAspGlnIleuSerPheMetSerValAlaLysThrArgValys 140
Db 1768 ATTGCCAAGAGTTGACAGAGAGAGAGCTTCATGAGCGGTGCCAAGCCAGAGTTAAG 1827
Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
Db 1828 CAGAGTTACGCCCTCTGCAAGTCTTTCTATTATTCACAGAGTTGGTTCAACTTTGGAGG 1887
Qy 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyYrArgYrAlaLeuLeuPhe 180
Db 1888 GAGCTCCGGCTGAGGCCCATCTGAGAGGATCGATGATATCGATATGCTCCCTGCTATT 1947
Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGlnAsn 200
Db 1948 GCTACCCAGAACCAATCATCGCCGATATGCTATTGAGCTGACAGCAGATATGGAGAT 2007
Qy 201 LysLeuIleHisGlyIleAlaGlnIleuLeuIleHisAlaArgArgGlnGlnIleLys 220

Db 2008 AATTTGATTCACGGATTCCTCAGAGATTTTAAATTCATCCGCTGACAGAGAAAGAA 2067

Qy 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239

Db 2068 TTCCCTTTGGTGGGGCCGACAGCTGTGGAAGCGTTTGAAGGACACCATTTGCAATG 2124

RESULT 4

US-09-545-334B-7
Sequence 7, Application US/09545334B
Patent No. 6992237

GENERAL INFORMATION:
APPLICANT: Zinselmeyer, Chris

APPLICANT: Haben, Jeff
APPLICANT: Tomes, Dwight

TITLE OF INVENTION: Regulated Expression of Genes in Plant
TITLE OF INVENTION: Seeds

FILE REFERENCE: 0803
CURRENT APPLICATION NUMBER: US/09/545,334B

CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/129,844

PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7

LENGTH: 5622
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Promoter and terminator from Zea mays as found in
OTHER INFORMATION: Genbank Accession #S78780; gene from Agrobacterium

OTHER INFORMATION: tumefaciens as found in Molecular and General
OTHER INFORMATION: Genetics 216:388-394 (1989).

US-09-545-334B-7

Alignment Scores:

| Pred. No.: | 3,3e-138 | Length: | 5622 |
|------------------------|--|---------------|------|
| Score: | 1230.00 <td>Matches:</td> <td>239</td> | Matches: | 239 |
| Percent Similarity: | 100.0% <td>Conservative:</td> <td>0</td> | Conservative: | 0 |
| Best Local Similarity: | 100.0% <td>Mismatches:</td> <td>0</td> | Mismatches: | 0 |
| Query Match: | 100.0% <td>Indels:</td> <td>0</td> | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-10-817-483-2 (1-239) x US-09-545-334B-7 (1-5622)

Qy 1 MetAapLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleala 20
Db 1525 ATGATCTACGCTAATTTTCGTCCTCACTGACAGAAAGACATCGACTCGATAGCT 1584
Qy 21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGln 40
Db 1585 CTGGCCAGCAGACAGCTGGCTCCAGTCTCTCGTCGATCGGCTCAATGCTGCTCTCA 1644
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyYThrThrArgLeuYr 60
Db 1645 CTATCAACCGGAAAGGGGAGCAACAGTGAAGAACTGAAGAAAGCACTGCTGTAC 1704
Qy 61 LeuAspAspArgProLeuValIysGlyIleIleThrAlaLysGlnAlaHisGlnArgLeu 80
Db 1705 CTGTGATCGCCCTTTGGTAAAGGATCATTTACAGCAACAGCTCATGACGGCTC 1764
Qy 81 IleAlaGlnValHisAsnHisGlnAlaLysGlyLysLeuIleLeuGlnGlySerIle 100
Db 1765 ATTTGGAGGTGCACAAATCACAGAGCCAAAGCGGGCTTATCTTGAGGAGGATCTATC 1824
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgYrTrpAsnAlaAspPheArgTrpHisIle 120
Db 1825 TCGTTGCTCAGGTGATGGCCGAAGTCTTATTGGAACGGCGATTTTCGTGGCATATT 1884
Qy 121 IleArgAsnGlnLeuAlaAspGlnIleuSerPheMetSerValAlaLysThrArgValys 140
Db 1885 ATTTGCCAAGAGTTGACAGAGAGAGAGCTTCATGAGCGGTGCCAAGCCAGAGTTAAG 1944

Qy 141 GImeUeuArpProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrrArg 160
|||
Db 1945 CAGATGTTACGCCCTCTGCAGGCTTCTATTTCCAAAGGTTGTTCACTTTGAGG 2004
Qy 161 GlnProArGleuArpProIleLeuGlyIleAspGlyTrrArgTrrAlaLeuPhe 180
|||
Db 2005 GAGCTCGGCTGAGGCCCTACTCGAAGGATTCATGATTCATATGCCCTCTATT 2064
Qy 181 AlaThrGlnAngInIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
2065 GCTACCCAGAACCATGATCAGCCGATATGCTATTGACGCTCGACGAGATATGAGAAAT 2124
Db 201 LysLeuIleHISGlyIleAlaGlnGluPheLeuIleHISAlaArgArgGlnGluGln 220
2125 AAAATTGATTCCAGGATTCGCTCAGAGATTCTTAATCCATGCGCGCTCGACAGAAACAGAA 2184
Qy 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
2185 TTCCCTTGGTGGCGCGACAGCTGTCGAAAGCGTTTGAAGAACCACTTCGAAATG 2241

RESULT 5

US-09-434-837-12
; Sequence 12, Application US/09434837
; Patent No. 6759574
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.,
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/09/434,837
; EARLIER FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 60/107,185
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-434-837-12

Alignment Scores:

Pred. No.: 2.97e-112 Length: 723
Score: 1005.00 Matches: 193
Percent Similarity: 88.7% Conservative: 19
Best Local Similarity: 80.8% Mismatches: 27
Query Match: 81.7% Indels: 0
Gaps: 0

US-10-817-483-2 (1-239) * US-09-434-837-12 (1-723)

Qy 1 MetAspLeuArGleuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
|||
Db 1 ATGAGCCCTGCATCTAATTTTGGTTCACACTTGCACAGAAAGACAGACACCGCGATACT 60
Qy 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspAlaGlnGlyCysProGln 40
|||
Db 61 CTGGCCGACAGAGGCGCTTCAGTCCCTTGGCTTGAATGCGTCCATGCTGCTCTAA 120
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTrr 60
|||
Db 121 CTATCAACCGAAGGAGGACCAACATGGAAGACTGAAAGAAACAGACGGCTTTCTAC 180
Qy 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHISGlnArgLeu 80
|||
Db 181 CTTGATGATCGGCGCTCTGGTGGAGGATTCATCGACGCAAGCTCATCATAGCGCTG 240
Qy 81 IleAlaGluValHISAsnHISGlnAlaLysGlyIleLeuIleLeuGlnGlySerIle 100
|||
Db 241 ATCGAGGAGGTGTTAATCATGAGGCAACGCGGCTTATCTTGAAGGAGATCCACC 300
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTrrTrrPasnAlaAspPheArgTrrHisIle 120
|||

Db 301 TCGTGTCTCACTGCATGAGGCGCGAAACAGCTATTGAGTGCAGATTTTCGTGGCATATT 360
Qy 121 IleArgAngInLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
|||
Db 361 ATTGCGCAAGATTACCGGACCAAGACACTTCTGAAAGCGCGCAAGCGCGAGTTAAAG 420
Qy 141 GImeUeuArpProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrrArg 160
|||
Db 421 CAGATGTTGACCCCGCTGAGGCCATTCCTATTCTTAAGATGGTGTTCCTTTGGAAT 480
Qy 161 GlnProArGleuArpProIleLeuGlnGlyIleAspGlyTrrArgTrrAlaLeuPhe 180
481 GAACCTCGGCTGAGGCCCATTCCTAAGAGATCATGATCATATGTCATGTCATGTTGTT 540
Qy 181 AlaThrGlnAngInIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
541 GCTAGCCAGAACCATGATCAGCCGATATGCTATTGACGCTTGCAGAAATATGAAAGCT 600
Qy 201 LysLeuIleHISGlyIleAlaGlnGluPheLeuIleHISAlaArgArgGlnGluGln 220
601 AAGTTGATTATGGATCGCTCAGAGATTTCTATCCATGCGCGCAACAGAAACAGAA 660
Db 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
661 TTCCCGCAAGTTACGACGCGCTTTCGACGATTCGAAGTCAATCCGTTGGAATG 717

RESULT 6

US-09-073-587-4
; Sequence 4, Application US/09073587
; Patent No. 6268552
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Transgenic Seedless Plants
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,587
; FILING DATE: 06-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/045,725
; FILING DATE: 06-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Feiber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 4-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..725
US-09-073-587-4

Alignment Scores:
Pred. No.: 3,1e-112 Length: 745
Score: 1005.00 Matches: 193
Percent Similarity: 88.7% Conservative: 19
Best Local Similarity: 80.8% Mismatches: 27
Query Match: 81.7% Indels: 0
Gaps: 0
DB: 3

US-10-817-483-2 (1-239) x US-09-073-587-4 (1-745)

Qy 1 MetaspAaArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIleAla 20
Db 3 ATGACCTGCACTTAATTTTCGATCCACTTCACAGGAAAGACGACCGCGATAGCT 62

Qy 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 63 CTGGCCAGACAGAGGGCTTCACATCTTTCCTTGTATCGGGTCCAAATGCTGCTCA 122

Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyThrThraArgLeuTyr 60
Db 123 CTATCAACCGGAAAGGAGACGACCAAGTGAAGAACTGAAGAAAGACGCGCTCTAC 182

Qy 61 LeuAspAaArgProLeuValLysGlyIleIleThraIalysGlnAlaHisGlnArgLeu 80
Db 183 CTTGATGATCGGCTCTGATGGAGGATATCATCGACCGCAAGCTCATATAGGCTG 242

Qy 81 IleAlaGlnValHisAsnHisGlnAlaLysGlyGlyLeuGlnGlyGlySerIle 100
Db 243 ATCGAGAGGAGGTATATATCATGAGGCCAAGCGGGCTTATTCAGAGGAGATCCACC 302

Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 303 TCGTTGCTCAACTGCATGCGCGGAAACAGCTATTGAGAGCAGATTTTCGTTGGCATATT 362

Qy 121 IleArgAsnGlnLeuAlaAspGlnGlnSerPheMetSerValAlaLysThrArgValLys 140
Db 363 ATTCGCCACAAAGTTACCCGACCAAGACCTTCATGAAGAACCGGCCAGAGTTAAG 422

Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
Db 423 CAGATGTTGACACCCGCTGACAGGCCATTTATTTATTCAGAGTTGTTATCTTTGAAAT 482

Qy 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 483 GAACCTCGCTGAGGCCCATCTGAAAGAGATCGATGATATCGATATGCCATGTTGTTT 542

Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGlnAsn 200
Db 543 GCTAGCCGAAACCGATACGCGCAGATATGCTATTGACGCTTGACGCAAAATATGGAAGT 602

Qy 201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLys 220
Db 603 AAGTTGATTAATGGATCGCTCAGAGATATTTCACTCCATGCCGCCAAGAGAAAGAAA 662

Qy 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
Db 663 TTCCCCCAAGTTAAACGACGCGCTTTCAGCGATTCGAAGGTCATCGCTCGAATG 719

RESULT 7
5428147-1
Patent No. 5428147
APPLICANT: BARKER, RICHARD F.; KEMP, JOHN D.
TITLE OF INVENTION: OCTOPINE T-DNA PROMOTERS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/91,538
FILING DATE: 13-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 869,216
FILING DATE: 13-APR-1992
APPLICATION NUMBER: 869,216
FILING DATE: 13-APR-1992

APPLICATION NUMBER: 440,432
FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 553,786
FILING DATE: 19-NOV-1983
APPLICATION NUMBER: 741,034
FILING DATE: 06-AUG-1991
APPLICATION NUMBER: 144,775
FILING DATE: 20-JAN-1988
APPLICATION NUMBER: 485,614
FILING DATE: 15-APR-1983
APPLICATION NUMBER: 713,624
FILING DATE: 10-JUN-1991
APPLICATION NUMBER: 260,574
FILING DATE: 21-OCT-1988
APPLICATION NUMBER: 848,733
FILING DATE: 01-APR-1986
APPLICATION NUMBER: 535,354
FILING DATE: 26-SEP-1983
SEQ ID NO:1:
5428147-1
LENGTH: 24595

Alignment Scores:
Pred. No.: 5,81e-110 Length: 24595
Score: 1005.00 Matches: 193
Percent Similarity: 88.7% Conservative: 19
Best Local Similarity: 80.8% Mismatches: 27
Query Match: 81.7% Indels: 0
Gaps: 0
DB: 10

US-10-817-483-2 (1-239) x 5428147-1 (1-24595)

Qy 1 MetaspAaArgLeuIlePheGlyProThrCysThrGlyLysThrSerThraIleAla 20
Db 8771 ATGACCTGCACTTAATTTTCGATCCACTTCACAGGAAAGACGACCGCGATAGCT 8830

Qy 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 8831 CTTCGCCAGACAGAGGGCTTCACATCTTTCGTTGATCGGGTCCAAATGCTGCTCA 8890

Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyThrThraArgLeuTyr 60
Db 8891 CTATCAACCGGAAAGGAGACGACCAAGTGAAGAACTGAAGAAAGACGCGCTTCTAC 8950

Qy 61 LeuAspAaArgProLeuValLysGlyIleIleThraIalysGlnAlaHisGlnArgLeu 80
Db 8951 CTTGATGATCGGCTCTGATGGAGGATATCATCGACCAAGCAAGCTCATATAGGCTG 9010

Qy 81 IleAlaGlnValHisAsnHisGlnAlaLysGlyGlyLeuGlnGlyGlySerIle 100
Db 9011 ATCGAGAGGAGGTATATATCATGAGGCCAAGCGGGCTTATTCGAGGAGATCCACC 9070

Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 9071 TCGTTGCTCAACTGCATGCGCGGCAAGCTATTGAGAGTTCGATTTGCGCATATT 9130

Qy 121 IleArgAsnGlnLeuAlaAspGlnGlnSerPheMetSerValAlaLysThrArgValLys 140
Db 9131 ATTCGCCACAAAGTTACCCGACCAAGACCTTCATGAAGAGGCGCAAGCCAGAGTTAAG 9190

Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
Db 9191 CAGATGTTGACACCCGCTGACAGGCCATTTCTATTTCAGAGTTGTTATCTTTGGAAT 9250

Qy 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 9251 GAACCTCGCTGAGGCCCATTTCTAAAGAGATCGATGATATCGATATGCCATGTTGTTT 9310

Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGlnAsn 200
Db 9311 GCTAGCCGAAACCGATACGCGCAGATATGCTATTGACGCTTGACGCAAAATATGGAAGT 9370

Qy 201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLys 220

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Db      9371 AAGTTGATTAATGGAATCGCTCAGAGATTTTCATCCATGCGCCCAACAGAAACAGAA 9430
Qy      221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
Db      9431 TTCCCCAAGATTACGACGCGCTTTCGACCGATTCCAGAGTCATCCGTTCCGATG 9487

RESULT 8
US-08-971-395-1
; Sequence 1, Application US/08971395
; Patent No. 6359197
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M
; APPLICANT: No. 6359197, Yoo-Sun
; APPLICANT: Gan, Susheng
; TITLE OF INVENTION: Transgenic Plants with Altered
; TITLE OF INVENTION: Senescence Characteristics
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,395
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.94908
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-971-395-1

Alignment Scores:
Pred. No.: 4,45e-110 Length: 3182
Score: 995.00 Matches: 192
Percent Similarity: 88.3% Conservative: 19
Best Local Similarity: 80.3% Mismatches: 28
Query Match: 80.9% Indels: 0
DB: 3 Gaps: 0

US-10-817-483-2 (1-239) x US-08-971-395-1 (1-3182)
Qy 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
Db 2181 ATGGAACCTGACATCAATTTTGGGTCCAACTTGCAACAGAAAGACACACACGCGATACCT 2240
Qy 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 2241 CTTGCCACGACAGACAGGCGCTTCCAGTCTTTCGCTGATCGGGTCCAAATCGTCTCCAA 2300
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLysGlyThrThrArgLeuTyr 60
Db 2301 CTATCAACCGGAAACGAGACCAACAGTGGAAAGAACTGAAAGGAACACACGCTCTTAC 2360
Qy 61 LeuAspAspArgProLeuValLysGlyLysIleLeuThrAlaLysGlnAlaHisGlnArgLeu 80
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Db      2361 CTTGATATATGCGCTCTGGTGGAGGATATCATCCCAACAGCAAGCTCATATAGGCTG 2420
Qy      81 IleAlaGlnValHisAsnHisGlnAlaLysGlyLeuIleLeuGlnGlySerIle 100
Db      2421 ATCGAGAGAGGTGTATATATCATGAGCCCAACGCGCGCTTATTTCTTGAGGAGATCCACC 2480
Qy      101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db      2481 TCGTGTCTCAACCTGACATGCGCGCAAGACGCTATTGGAGTGCAGATTTTCGTTGCCATATT 2540
Qy      121 IleArgAsnGlnLeuAlaAspGlnGluSerPheMetSerValAlaLysThrArgValLys 140
Db      2541 ATTGCCACAAAGTTACCCGACCAAGACACCTTCTATGAAAGCGCCCAAGCCGACGATTAG 2600
Qy      141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTyrArg 160
Db      2601 CAGATGTTGACCCCGCTGGAGGCCATTCTATTATTCAGAGTTGTTTATCTTTGGCAT 2660
Qy      161 GlnProArgLeuArgProIleLeuGlnGlyLysAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db      2661 GAACCTCGGCTGAGGCCCATTTCTGAAAGATCGATGATATGATATGCGATGTGTTT 2720
Qy      181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
Db      2721 GCTAGCCAGAACGATCAGACGCGCAGATATGCTATTCAGCTTGACCGCAAAATATGGAAGT 2780
Qy      201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLys 220
Db      2781 AAGTTGATTAATGGAATCGCTCAGAGATATTTTCATCATGCGGCCCAACAGAAACAGAA 2840
Qy      221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
Db      2841 TTCCCCAAGTTAAGCAGCGCGCTTTCGACGAGTTCAGAGGTCATCCGTTCCGATG 2897

RESULT 9
US-09-434-837-5
; Sequence 5, Application US/09434837
; Patent No. 6759574
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.
; TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/09/434,837
; EARLIER FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 60/107,185
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-434-837-5

Alignment Scores:
Pred. No.: 6,72e-111 Length: 747
Score: 994.00 Matches: 191
Percent Similarity: 88.6% Conservative: 19
Best Local Similarity: 80.6% Mismatches: 27
Query Match: 80.8% Indels: 0
DB: 3 Gaps: 0

US-10-817-483-2 (1-239) x US-09-434-837-5 (1-747)
Qy 3 LeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAlaLeuAla 22
Db 18 CTGAATCAATTTTTCGGTCCAACTTGCAACGAAAGACGAGACCGGATGCTCTTGCC 77
Qy 23 GlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSer 42
Db 78 CAGCAGACAGGCGCTTCCAGTCTTTCGCTGATCGGGTCCAAATCGTCTCAACTATCA 137
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43 ThrGlySerGlyAArgProThrValGluGluLeuLeuGlyThrThrArgLeuLeuThrLeuasp 62
138 ACCGGAACCGGACGACCAAGCTGAGAGAACTGAAAGGAAACGACCGCTCTACCTTAT 197
63 AspArgProLeuValGlyGlyLeuThrAlaArgGlnAlaHisGluArgLeuLeuLea 82
198 GATCGGCTCTGATGAGGATATCATCGACGCAAGCAAGCTCATCATGAGCTGATCGAG 257
83 GluValHisAsnHisGluAlaValGlyLeuLeuLeuGluGlyGlySerLeuSerLeu 102
258 GAGGTGTTAATCATGAGGCGCAACGCGGCTTATCTTGAGGAGGATCCACCTCGTTG 317
103 LeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTyrHisIleLeaArg 122
318 CTCAACTGCTGATGCGCGCAACAGCTATTGAGTGCAGATTTTCTTGCGATTTATTCGC 377
123 AsnGluLeuAlaAspGluGluSerPheMetSerValAlaValThrArgValIleGlnMet 142
378 CACAAGTTAACCGACCAAGAGACCTTCATGAAAGCGCCCAAGCCAGAGTTAAGCAGATG 437
143 LeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArgGluPro 162
438 TTGCACCCCGCTGCGAGGCCATTCTATTTCAAGAGTTGTTATCTTTGGAATGAACT 497
163 ArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPheAlaThr 182
498 CGGCTGAGGCGCATCTGTAAGAGATGATGATGATGATGATGATGATGATGATGATGATG 557
183 GlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAlaAspMetGluAsnIleLeu 202
558 CAGAACCGAGATCAGCGAGATATGCTATTGACGCTTGAACGCAAAATGGAAGTAAAGTG 617
203 IleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluIleAspPhePro 222
618 ATTAATGGATGCTCAGAGATTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 677
223 LeuValGlyAlaThrAlaValAlaPheGluGlyProProPheArgMet 239
678 CAACTTAACGACGCGCTTTCAGCGAGATTCGAAGGCTCATCCGTTGCGAATG 728

RESULT 10
US-08-413-135-1
; Sequence 1, Application US/08413135
; Patent No. 5689042
; GENERAL INFORMATION:
; APPLICANT: Amasino, Richard M
; TITLE OF INVENTION: Transgenic Plants with Altered
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,135
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296.92808
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3183 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "SAG12-1 Promoter DNA"
US-08-413-135-1
Alignment Scores:
Pred. No.: 9.6e-109 Length: 3183
Score: 984.00 Matches: 190
Percent Similarity: 88.2% Conservative: 19
Best Local Similarity: 80.2% Mismatches: 28
Query Match: 80.0% Indels: 0
DB: 2 Gaps: 0
US-10-817-483-2 (1-239) x US-08-413-135-1 (1-3183)
3 LeuArgLeuIlePheGlyProThrCysThrGlyThrSerThrAlaIleAlaLeuAla 22
2188 CTGCATCTAATTTTCGTCCTCACTTGCACAGAGAAAGAGACGACCGGATAGCTTCC 2247
23 GlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSer 42
2248 CAGCAGACAGGCGCTTCAGCTCTTCGCTGATCGGCTCATCGTCTCATCACTATCA 2307
43 ThrGlySerGlyAArgProThrValGluGluLeuLeuGlyThrThrArgLeuLeuThrLeuasp 62
2308 ACCGGAACCGGACGACCAAGCTGAGAGAACTGAAAGGAAAGACGCGCTCTCACTTAT 2367
63 AspArgProLeuValGlyGlyIleIleThrAlaArgGlnAlaHisGluArgLeuLeuLea 82
2368 GATCGGCTCTGATGAGGATATCATCGACCGCAAGACGCTCATAGGCTGATCGAG 2427
83 GluValHisAsnHisGluAlaValGlyLeuLeuLeuGluGlyGlySerLeuSerLeu 102
2428 GAGGTGTTAATCATGAGGCGCAACGCGGCTTATCTTGAGGAGATTCACCTCGTTG 2487
103 LeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTyrHisIleLeaArg 122
2488 CTCAACTGCTGATGCGCGCAACAGCTATTGAGTGCAGATTTTCTTGCGATTTATTCGC 2547
123 AsnGluLeuAlaAspGluGluSerPheMetSerValAlaValThrArgValIleGlnMet 142
2548 CACAAGTTAACCGACCAAGAGACCTTCATGAAAGCGCCCAAGCGCTTAAGCAGATG 2607
143 LeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArgGluPro 162
2608 TTGCACCCCGCTGACGCGCATTTATTTCAAGGTTGTTATCTTTGGAATGAACT 2667
163 ArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPheAlaThr 182
2668 CGGCTGAGGCGCATTCGAAAGAGATCGATGATATCATATGCTATTTGCTGATGC 2727
183 GlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAlaAspMetGluAsnIleLeu 202
2728 CAGAACCGAGATCAGCGAGATATGCTATTGACGCTTGAACGAATATGGAAGTAAAGTG 2787
203 IleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluIleAspPhePro 222
2788 ATTAATGGATGCTCAGAGATTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 2847
223 LeuValGlyAlaThrAlaValAlaPheGluGlyProProPheArgMet 239
2848 CAACTTAACGACGCGCTTTCAGCGAGATTCGAAGGCTCATCCGTTGCGAATG 2898

RESULT 11
US-09-434-837-9
; Sequence 9, Application US/09434837
; Patent No. 6759574

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: GENERAL INFORMATION:
: APPLICANT: Ream, Walt et al.,
: TITLE OF INVENTION: Plants Having Enhanced Gall Resistance and
: FILE REFERENCE: 53629
: CURRENT APPLICATION NUMBER: US/09/434,837
: EARLIER FILING DATE: 1999-11-04
: EARLIER APPLICATION NUMBER: 60/107,185
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 9
: LENGTH: 2544
: TYPE: DNA
: ORGANISM: Agrobacterium tumefaciens
: US-09-434-837-9

Alignment Scores:
Pred. No.:      8,23e-73      Length:      2544
Score:          686.50      Matches:      191
Percent Similarity: 25.2%      Conservative: 20
Best Local Similarity: 22.8%      Mismatches: 26
Query Match:    55.8%      Indels:      599
DB:             3      Gaps:      1

US-10-817-483-2 (1-239) x US-09-434-837-9 (1-2544)

QY      3      LeuAArgLeuIlePheGlyProThrCysThrGlyIleThrSerThrAlaIleAlaLeuA 22
Db      18      CTGATCATTAATTTTCGGTCCAACTTGACAGAAAGACGACCGCATAGCTTGGCC 77
QY      23      GlnGlnThrGlyLeuProValLeuSerLeuSparGValGlnCysCysProGlnLeuSer 42
Db      78      CAGAGAGAGGGCTTCGATCGCTTCGCTGATCGGTCGTCATGCTGCTCAACTATCA 137
QY      43      ThrGlySerGlyAArgProThrValGlnIleLeuIleGlyIleThrArgLeuTyrLeuAsp 62
Db      138      ACCGGAACCGGACCAACCAAGGTGMAAAGTGAAGAACGACCGCTCTCACTTGAT 197
QY      63      AspArgProLeuValIleGlyIleIleThrAlaIleGlnAlaIleGlnArgLeuIleAla 82
Db      198      GATCGGCTCTGTTGGAGGGTATCATCGACCAAGCTCATGAGCTGATCGAG 257
QY      83      GluValHisAsnHisGluAlaIleGlyIleLeuGlnIleGlySerIle----- 100
Db      258      GAGGTGATTAATCATGAGGCCAAGCGGCTTATCTTGAGGAGGATTCATGTCATGA 317
QY      100      ----- 100
Db      318      ACCTCTCTTGATTAACGAGTGCATCTCCCAACCAAAATGGTGAATCGACATGCT 377
QY      100      ----- 100
Db      378      CGATTAAGCGGATGAATGACCGCAGGGTTCCGATGCTTCTTAGAACGAGAAGCTTC 437
QY      100      ----- 100
Db      438      TAGGGGAAGAGATTACTCAAGCTCCACGAGTGACGCGCTGGGTTAGCTTGCAAAAG 497
QY      100      ----- 100
Db      498      GCTGGCCGATGGTGGCTTCCCGAGATCTCAAGCTGTGTGAAAGGTAGCAGTTCTCTCCG 557
QY      100      ----- 100
Db      558      TTATATCTATATTGGCAAAGAATCTGGGGCGGATACTGAATCGAAACCTTGCGCGCG 617
QY      100      ----- 100
Db      618      GGCACAGCTAGTGTCTGTTGCCATGCACTTGACACCAATTGGCATGATTTCTCCGA 677
QY      100      ----- 100
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Db      678      AGCACTAATATCCAGCCCTGTTTTTGTGAGCGGTAAAGATGTGCACCGATTGATCT 737
QY      100      ----- 100
Db      738      TAGCATTTGGTGGCCATTTCATCTTAAGACTCGCGGTTTGCAACCTGCCAATGCC 797
QY      100      ----- 100
Db      798      GCTGTACGAAATGGCAGATGAAATCGTTACGGGTTTACCATTAACCTTGAAGGGCC 857
QY      100      ----- 100
Db      858      CGTGCATTTGACATGGTAGCTTATGGTCGAAACCTGATGCTGAAGGTTCCGAGGTTCC 917
QY      100      ----- 100
Db      918      CTTTCAACAATCGACTTGTGCTTACGACTGCAGACCGTTTTTTGACCAATGTTCCGATAG 977
QY      100      ----- 100
Db      978      TGAAGGATGGGCTTCTTCCGAGAGATGTTCTTAAGCCGAAAGTGGCGGTCATTGGCGC 1037
QY      100      ----- 100
Db      1038      TGGCATTTCCGACTCGTGGTGGCAAGAACTGCTTCATGCTGGGGTGAACGATGTTAC 1097
QY      100      ----- 100
Db      1098      AATATATGAAGCAGATGATCGTGTGAGGCAAGCTTTGTCATGCTTTACAGGACGC 1157
QY      100      ----- 100
Db      1158      TCCTAGTGTGTGGCCGAATGGGGCGGATGCCATTTCTCTGCTGCAATTTGCTTGT 1217
QY      100      ----- 100
Db      1218      TTTCTTCGAGCGTTACGGCTGCTCTTGATGAGCGGTTCCCAATCCCGACAGT 1277
QY      100      ----- 100
Db      1278      CGACACTTACTGTGCTACCAAGCGTCCAATACATGTGAAAGCCGGGACGTCGACCC 1337
QY      100      ----- 100
Db      1338      GAAGCTGTCATCGCGCTTACAAAGGTGGCGGCTTCTTGAAGACGTTTTCATGA 1397
QY      100      ----- 100
Db      1398      GCGATATATTGTGTGGCTTCGCTGCTATTACTCAGGCTTGAATCAGGACAT 1457
QY      100      ----- 100
Db      1458      TAGTGGGCTCATGACTCTGGCAAAATTTGGCTGAACCGTTTCGGAGGAGTCTTCTC 1517
QY      100      ----- 100
Db      1518      TTCAGGATAGAGGATCTTTTCTGGCACAATCTCTGCTGTGTAACATGAGTTT 1577
QY      100      ----- 100
Db      1578      CCTCATGATTGGACCTATTCAAGCTAATGGAATAGATCTGGCGGGTTTGTCCAGT 1637
QY      100      ----- 100
Db      1638      TTTTGAAGCGGGTTTATAGATCTCCGCTGGTCATCAACGATATGAAGAAATCA 1697
QY      100      ----- 100
Db      1698      GCGATGTGCCCTGAAGGAATCTGAAATTCCACGTCGGAATCGCATCTGAAGTGTTAA 1757
QY      100      ----- 100
Db      1758      CGGTGTCTGTGAGCGCAGCATATGCAATGTTCAAGTCAGGGCGATTGGAAGAAAA 1817
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| | | | |
|--|------|---|------|
| Qy | 100 | ----- | 100 |
| Db | 1818 | GACAAAAATAAGATAGGCTTAAAGCGGAGTATCTGAACCTTATGATTAAGGTGCTG | 1877 |
| Qy | 100 | ----- | 100 |
| Db | 1878 | CACATCTTGACTCGCAAAATATCAACTAGGATTCCTGACATGCGATACCAATATTTT | 1937 |
| Qy | 100 | ----- | 100 |
| Db | 1938 | TCAGGACACAGTGAACCAAGCGTTGATTAACAGCCATATGACAGGATCGTCAAACTCTT | 1997 |
| Qy | 100 | ----- | 100 |
| Db | 1998 | CCTGATGACTGAACGAAAAATTCGTGTAGACCATATCCTCCCGTCTTGTCCTCATGGA | 2057 |
| Qy | 101 | ----- | 103 |
| Db | 2058 | CGGATCGCAAAAGACAGTGTATTCGCTGACTATGATGTCGAGATCCACCTCGTGTCTC | 2117 |
| Qy | 104 | ArgCysMetAlaGlnSerArgTyrTTrpAsnAlaArgPheArgTyrPheIleIleArgAsn | 123 |
| Db | 2118 | AACGTCATGCGCGCAAAACAGCTATTTGGAGTGCAGATTTTCGTTCGATATTATTCGCCAC | 2177 |
| Qy | 124 | GluPheAlaAspGluGlnSerPheMetSerValAlaLysThrArgValIleGlnMetLeu | 143 |
| Db | 2178 | AAGTATCCCGACCAAGACACCTTCTATGAAAGCGCCAAAGCCAGAGTTTAAGCAGATGTG | 2237 |
| Qy | 144 | ArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTyrArgGluProArg | 163 |
| Db | 2238 | CACCCCGCTGACGGCATTTCTATTATTAACAAGTTGGTTTATCTTTGGAAATGAACCTCGG | 2297 |
| Qy | 164 | LeuArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPheAlaThrGln | 183 |
| Db | 2298 | CTGAGGCCCATCTGAAAGAGATCGATGGAATGATGATGTCATGTTGTGCTAGCCAG | 2357 |
| Qy | 184 | AsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsnLysLeuIle | 203 |
| Db | 2358 | AACACGATCAGCGCAGATATCTTATTCGACCTTGACGCAAAATATGGAAGTGAATGATT | 2417 |
| Qy | 204 | HisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnLysPheProLeu | 223 |
| Db | 2418 | AATGGGATCGCTCAGAGTATTTTCATTCATCGCGCCAAACAGAAATTCGCCCAA | 2477 |
| Qy | 224 | ValGlyAlaThrAlaValGluAlaPheGlnGlyProProPheArgMet | 239 |
| Db | 2478 | GTTAACGACGCGCTTTCGACGAGTATCGAAGGTCAATCCGTTCCGAATG | 2525 |
| RESULT 12 | | | |
| US-08-054-985-2 | | | |
| Sequence 2, Application US/08054985 | | | |
| Patent No. 5496732 | | | |
| GENERAL INFORMATION: | | | |
| APPLICANT: Smigocki, Ann C | | | |
| APPLICANT: Neal Jr, John W | | | |
| TITLE OF INVENTION: ENHANCED INSECT RESISTANCE IN PLANTS | | | |
| TITLE OF INVENTION: GENETICALLY ENGINEERED WITH A PLANT HORMONE GENE | | | |
| TITLE OF INVENTION: INVOLVED | | | |
| TITLE OF INVENTION: IN CYTOKININ BIOSYNTHESIS | | | |
| NUMBER OF SEQUENCES: 3 | | | |
| CORRESPONDENCE ADDRESS: | | | |
| ADDRESSEE: Janelle S. Graeter | | | |
| STREET: Room 411, Building 005, BARC-W | | | |
| CITY: Beltsville | | | |
| STATE: Maryland | | | |
| COUNTRY: United States of America | | | |
| ZIP: 20705 | | | |
| COMPUTER READABLE FORM: | | | |
| MEDIUM TYPE: Floppy disk | | | |
| COMPUTER: IBM PC compatible | | | |
| OPERATING SYSTEM: PC-DOS/MS-DOS | | | |
| SOFTWARE: PatentIn Release #1.0, Version #1.25 | | | |

| | |
|----|--|
| : | CURRENT APPLICATION DATA: |
| : | APPLICATION NUMBER: US/08/054,985 |
| : | FILING DATE: 30-APR-1993 |
| : | CLASSIFICATION: 800 |
| : | ATTORNEY/AGENT INFORMATION: |
| : | NAME: Graeter, Janelle S |
| : | REGISTRATION NUMBER: 35024 |
| : | REFERENCE/DOCKET NUMBER: 015.92 |
| : | TELECOMMUNICATION INFORMATION: |
| : | TELEPHONE: (301) 504-6629 |
| : | TELEFAX: (301) 504-5060 |
| : | INFORMATION FOR SEQ ID NO: 2: |
| : | SEQUENCE CHARACTERISTICS: |
| : | LENGTH: 584 base pairs |
| : | TYPE: nucleic acid |
| : | STRANDEDNESS: single |
| : | TOPOLOGY: linear |
| : | MOLECULE TYPE: DNA (genomic) |
| : | HYPOTHETICAL: NO |
| : | ANTI-SENSE: NO |
| : | ORIGINAL SOURCE: |
| : | ORGANISM: Agrobacterium tumefaciens |
| : | US-08-054-985-2 |
| : | |
| : | Alignment Scores: |
| : | Pred. No.: 4,61e-58 Length: 584 |
| : | Score: 557.00 Matches: 145 |
| : | Percent Similarity: 67.7% Conservative: 12 |
| : | Best Local Similarity: 62.5% Mismatches: 28 |
| : | Query Match: 45.3% Indels: 49 |
| : | DB: 2 Gaps: 6 |
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| Oy | 1 MetAspLeuArgIeuIlePheGlyProThrCysThrGlyLysThrSerThralIeAla 20 |
| Dd | 1 ATGACCTGCATCTAATTTCGGTCAAACTTGACAGAAAAGACAGACACCGCATACT 60 |
| Oy | 21 LeuAlaGlInGIlnThrgLyLeuBroValIeuSerIeuAparg-ValGincyCySprogl 40 |
| Dd | 61 CTGGCCACAGACAGACAGG-----CTGGGTCCAATGCTGTCTCA 99 |
| Oy | 40 nLeuSerThrgLysSerGlyValrgProThrValGIuGIuLeuLysGlyThrrTrargleuty 60 |
| Dd | 100 ACTATCAACCGGAAGCGACGACCAACGTGGAMAACATGAAAGAAGACGCCCTCTTA 155 |
| Oy | 60 rIeuAapApargProLeuValLys-GlyIleIleThraIalYsgIahIasgiuarql 80 |
| Dd | 160 C-----GGAGGGATCATGCGACGACCAGCACGCTCATATAGGC 199 |
| Oy | 80 euIleAagiuaIHisAenHIsigualalySgly-GlyLeuIleLeuglIgLyser 99 |
| Dd | 199 TGAITCAGGAGGTATATATCATGAGGCCAACGGGGGCTTA----- 240 |
| Oy | 100 lIleSerLeuLeuArgCysMetAlaGlnSerArgrLyrrTPaenalaaApPneArgrTpHis 119 |
| Dd | 241 ----TCGTTGCTCAACGTCAATGCGCGGAAGAAGCTATTGAGTGCAGATTTCGTTGCAT 297 |
| Oy | 120 lleIIeaArgAnsgIuIeuAalaSpdluIuIsePhmetSerValAla-LysThrArgVa 139 |
| Dd | 298 ATTATTCGCCACAGTTACCCGAC-----GGCCAAAGGCCAAGT 338 |
| Oy | 139 llys-GlnmetLeuArgProSerAlaGlyLeuSerIleIlglnGIuLeuValGlnLeut 155 |
| Dd | 337 TAAGCAGATGTTGCACCCCCCTGAGGCCATTTCTATTATCA-GAGTGGTTTTATCTTT 395 |
| Oy | 159 rParGluProArgLeuArgProIlleLeuglIgLyllaeBgLyTYrarqTyralLeul 179 |
| Dd | 396 GGAA-----TTTCTGAAGAAGATCGATGATTCGATTCGATGCCCATGT 436 |
| Oy | 179 euPheAlaThrGlnIuEnGlnIleThrProaApPmetLeuEglnIueAplaaSpnetG 199 |
| Dd | 437 TGGTTCGACCAAGAACGATCAAGCGCAGATATGCTATATG----- 477 |

Db 7617 ATCGGACGGCGAAGCCCTCTCCGAGAGGCTGGCTGCGGCTGCTCATCATCTGTGTC 7558
Qy 54 ----- 54
Db 7557 GCGGTGACCCGATGAGGCGTTCTCCGCTGTGATACACAGCCGCTGCGGACGCGCTC 7498
Qy 55 ----- GlyThrArgLeuYr 60
Db 7497 ATCGGAGATTGCGCACGCGCGCTGTCTTGTGTGTGGTGCGACCGGCTGTAT 7438
Qy 61 LeuAapAapAProLeuVallysglyleilethAlaLylsGlnAlaHlsGlnArgLeu 80
Db 7437 TGG-----CGCGTGTGCTTCACGTTGTGTGAGGCGCCCGCGGCTTGTCCGAGTTG 7384
Qy 81 IleAlaGluValHis-----AenHlsGluAlaLysGlyGlyLeuIleLeuGlu 96
Db 7383 AGGCGGAGCTGAGGCGCTGCGCGCGGTGAGGG-GCCGAGGCGGCTGATCGAGGCT 7325
Qy 97 Gly-----GlySerIleSerLeuLeuArgCysMetAlaGlnSerArg 110
Db 7324 GCGGAGGTGACCGCGAGACGGCGCGA-AGCTTCTCTCCG-----AGG 7281
Qy 111 TyrTPAaAlaAspPhe---ArgTPHlsIleIleArgAsnGluLeuAlaAspGluGlu 129
Db 7280 ACCTGTCGCGCTCATCCGCGGCTGAGATTCAATCCGACAGGCG-GTGCCCGCTCG 7222
Qy 130 SerPheMetSerValAlaLysThrArgVallysglnMetLeuArgProSerAlaGlyLeu 149
Db 7221 GCGTTC-----CGAAGGCCCATGCGCTTC 7198
Qy 150 SerIleIleGlnGluLeuValGlnLeuTPArgGluProArgLeuArgProIleLeuGlu 169
Db 7197 GCGCGGACCGCTATCCCTTCACATGTAAGTTCTGTGCGCACCGCGGACGTGCTATC 7138
Qy 170 GlyIleAspGlyTyrArgTyrAlaLeuLeuPheAlaThr---GlnAsnGlnIleThrPro 188
Db 7137 GGGCTCATCAACACCGCGACGCGGATGTTTCGAGCGTGTCTGAGGAGACCGCCG 7078
Qy 189 AspMetLeu-----LeuGln 193
Db 7077 GAGCTGCTGCGCGCGGCGGATGCGCCGATGCGCCATGCGAGCGTGGCTATGTCCAG 7018
Qy 194 LeuAapAlaAspMetGluAsnLysLeu-----IleHisGlyIleAlaGln 208
Db 7017 GCGCGCGCGCTGTTGAGGGGGGATGACGCGGAGAGAGGCGATTACAGACCGCGAG 6958
Qy 209 GluPheLeuIleHisAlaArgArgGln-----GluGlnLysPheProLeuValGly 225
Db 6957 GAGACGCGCGCTAGCGCAAGCGGAGTTGACGTGTCTCCGGAAGAGAGCC-----GGG 6904
Qy 226 AlaThrAlaValGluAlaPheGluGlyProPhe 237
Db 6903 GCT-----GTTCTTCTGCTCCCGCGTAC 6880

RESULT 15
US-09-602-787A-277
Sequence 277, Application US/09602787A
Patent No. 6696561
GENERAL INFORMATION:
APPLICANT: Pompeius, Mark
APPLICANT: Krueger, Burkhard
APPLICANT: Schuder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberbauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
FILE REFERENCE: BGI-125CP
CURRENT APPLICATION NUMBER: US/09/602,787A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USSN 60/141031
PRIOR FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931563.9
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932122.1
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932124.8
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932180.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932182.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932190.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932191.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932209.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932212.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932227.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932228.7
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932229.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932927.3
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940765.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940832.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940833.5
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941378.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941395.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942077.7
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942078.5
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942079.3
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 678
SEQ ID NO 277
LENGTH: 1026
TYPE: DNA
ORGANISM: Corynebacterium glutamicum

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus.p2n model

Run on: June 26, 2006, 20:05:52 ; Search time 1277 Seconds
(without alignments)

3449.583 Million cell updates/sec

Title: US-10-817-483-2

Perfect score: 1230

Sequence: 1 MDRLIFGPTCTGKTSTAIA.....KPLVGAATVAEFGPPPPM 239

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/abs/ABSSWEB.apool/US10817483/runat.26062006.142803.19017/app.query.fasta.1
-DB=Published_Applications_NA_Main -QFMT=fastcap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPEX=0 -UNITIS=bits -START=1 -END=-1
-MATRIX=bloum62 -TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs05h
-USER=US10817483 @CGN 1.1 1675 @runat.26062006.142803.19017 -NCPUs=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*

1: /EMC_Celerra_SIDS3/prodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/prodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/prodata/2/pubpna/US09A_PUBCOMB.seq:*
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9: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/prodata/2/pubpna/US10E_PUBCOMB.seq:*
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14: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/prodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | ID | Description |
|------------|-------|--------------|-----|---------------------|
| 1 | 1230 | 100.0 | 717 | US-10-369-493-38935 |

| | | | | |
|----|-------|-------|------|---------------------|
| 2 | 1230 | 100.0 | 723 | US-10-409-701-2 |
| 3 | 1230 | 100.0 | 1919 | US-10-817-483-1 |
| 4 | 1230 | 100.0 | 2722 | US-11-139-461-8 |
| 5 | 1230 | 100.0 | 2722 | US-11-139-461-9 |
| 6 | 1230 | 100.0 | 3017 | US-11-139-461-12 |
| 7 | 1230 | 100.0 | 5622 | US-11-139-461-7 |
| 8 | 1075 | 87.4 | 720 | US-10-369-493-35042 |
| 9 | 1075 | 87.4 | 720 | US-10-369-493-38138 |
| 10 | 1075 | 87.4 | 720 | US-10-369-493-38549 |
| 11 | 1075 | 87.4 | 720 | US-10-369-493-38954 |
| 12 | 1075 | 87.4 | 723 | US-10-821-711-2 |
| 13 | 1068 | 86.8 | 723 | US-11-156-084-1 |
| 14 | 1068 | 86.8 | 723 | US-11-156-084-20 |
| 15 | 1066 | 86.7 | 720 | US-10-369-493-38969 |
| 16 | 1052 | 85.5 | 720 | US-10-369-493-38968 |
| 17 | 1052 | 85.5 | 1997 | US-10-465-008-1 |
| 18 | 1050 | 85.4 | 720 | US-10-369-493-38949 |
| 19 | 1050 | 85.4 | 720 | US-10-369-493-38953 |
| 20 | 1050 | 85.4 | 723 | US-11-156-084-16 |
| 21 | 1050 | 85.4 | 723 | US-11-156-084-18 |
| 22 | 1035 | 84.1 | 777 | US-10-369-493-38971 |
| 23 | 1005 | 81.7 | 720 | US-10-369-493-38936 |
| 24 | 1005 | 81.7 | 720 | US-10-369-493-38940 |
| 25 | 1005 | 81.7 | 720 | US-10-369-493-38964 |
| 26 | 1005 | 81.7 | 720 | US-10-369-493-38966 |
| 27 | 1005 | 81.7 | 723 | US-10-187-339-12 |
| 28 | 1005 | 81.7 | 1988 | US-10-363-723-2 |
| 29 | 1005 | 81.7 | 2595 | US-10-369-324-3 |
| 30 | 1005 | 81.7 | 2595 | US-10-392-301-3 |
| 31 | 1005 | 81.7 | 2595 | US-10-607-538-3 |
| 32 | 1005 | 81.7 | 2595 | US-10-667-145-3 |
| 33 | 1005 | 81.7 | 2595 | US-10-505-079-3 |
| 34 | 1005 | 81.7 | 9323 | US-10-369-324-4 |
| 35 | 1005 | 81.7 | 9323 | US-10-607-538-4 |
| 36 | 1005 | 81.7 | 9323 | US-10-505-079-4 |
| 37 | 994 | 80.8 | 747 | US-10-187-339-5 |
| 38 | 984 | 80.0 | 3183 | US-10-072-077A-1 |
| 39 | 984 | 80.0 | 3183 | US-11-154-865-1 |
| 40 | 826 | 67.2 | 559 | US-10-369-493-37835 |
| 41 | 686.5 | 55.8 | 2544 | US-10-187-339-9 |
| 42 | 605.5 | 49.2 | 729 | US-10-369-493-38941 |
| 43 | 603.5 | 49.1 | 729 | US-10-369-493-35046 |
| 44 | 603.5 | 49.1 | 729 | US-10-369-493-38270 |
| 45 | 603.5 | 49.1 | 729 | US-10-369-493-38608 |

ALIGNMENTS

RESULT 1
US-10-369-493-38935
; Sequence 38935, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38935
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; US-10-369-493-38935
Alignment Scores:

Pred. No.: 3.78e-149 Length: 717
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-817-483-2 (1-239) x US-10-369-493-38935 (1-717)

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OY 1 MetaspLeuAArgLeuIlePheGlyProThrCySerThrglyLysThrSerThrAlaIleAla 20
Db 1 ATGATCTACGCTTAATTTTCGGTCCACTTGACAGAGAAAGACATGACATGCGATAGCT 60
OY 21 LeuAaglIngnInThrglyLeuProValLeuSerLeuAspArgValGlnCySerProGln 40
Db 61 CTTCGCCAGCAGACTGGCTCCCTCCAGTCTCTCGCTCGATCGCATTAATGCTGCTCTCAA 120
OY 41 LeuSerThrglySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
Db 121 CTATCAACCGAAGCGGCGCAGCAACAGTGAAGAACTGAAAGACATCGCTCTGAC 180
OY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db 181 CTGATGATCCCTTTGGTAAAGGATCATTAACGCCAAGCAAGCTCATGAACGGCTC 240
OY 81 IleAglValHisAsnHisGluAlaLysGlyIleLeuIleLeuGlnGlyIleSerIle 100
Db 241 ATTCGGAGGAGTGCAACATCAAGAGCGCAAGCGGCTTATCTTGAAGGAGATCTATC 300
OY 101 SerLeuLeuAArgCySerMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 301 TCGTTGCTCAGTGTGATGCGCCAAAGTCTTATTCGAACCGCGATTTTCGTTGGCATATT 360
OY 121 IleArgAsnGluLeuAlaAspGluGlnSerPheMetSerValAlaLysThrArgValLys 140
Db 361 ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGACGCGGCCAAGCAGAGATTAG 420
OY 141 GlnMetLeuAArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
Db 421 CAGATGTTACGCCCTCTGCAGGCTTCTTATTAACAAGATGGTTCACCTTGGAGG 480
OY 161 GluProArgLeuAArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 481 GAGCTCGGCTGAGGCGCATCTGGAAGGATCGATGATTCGATATGCCCTGCTATT 540
OY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 541 GCTACCCAGAACCGATCAACGCCCGATATGCTATTGCACTCGACGATATGAGAAAT 600
OY 201 LysLeuIleHisGlyIleAglIngnInPheLeuIleHisAlaArgArgGlnGlnLys 220
Db 601 AAATTGATTACGGTATCGCTCAGAGTTTCTTAATCCATGGCGCTGACAGAAACAGAA 660
OY 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
Db 661 TTCCTTTGGTGGGCGGACAGCTGTGAAAGCGTTTGAAGCAACCATTTGGAATG 717
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RESULT 2

US-10-409-701-2
; Sequence 2, Application US/10409701
; Publication No. US20030221224A1
; GENERAL INFORMATION:
; APPLICANT: Zinsmeister, Chris
; APPLICANT: Helenjarris, Timothy G.
; TITLE OF INVENTION: Enhanced Silk Exsersion Under Stress
; FILE REFERENCE: 1421
; CURRENT APPLICATION NUMBER: US/10/409,701
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,796
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

LENGTH: 723
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(720)
US-10-409-701-2

Alignment Scores:

Pred. No.: 3.82e-149 Length: 723
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-817-483-2 (1-239) x US-10-409-701-2 (1-723)

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OY 1 MetaspLeuAArgLeuIlePheGlyProThrCySerThrglyLysThrSerThrAlaIleAla 20
Db 1 ATGATCTACGCTTAATTTTCGGTCCACTTGACAGAGAAAGACATGACATGCGATAGCT 60
OY 21 LeuAaglIngnInThrglyLeuProValLeuSerLeuAspArgValGlnCySerProGln 40
Db 61 CTTCGCCAGCAGACTGGCTCCCTCCAGTCTCTCGCTCGATCGCATTAATGCTGCTCTCAA 120
OY 41 LeuSerThrglySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
Db 121 CTATCAACCGAAGCGGCGCAGCAACAGTGAAGAACTGAAAGACATCGCTCTGAC 180
OY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db 181 CTGATGATCCCTTTGGTAAAGGATCATTAACGCCAAGCAAGCTCATGAACGGCTC 240
OY 81 IleAglValHisAsnHisGluAlaLysGlyIleLeuIleLeuGlnGlyIleSerIle 100
Db 241 ATTCGGAGGAGTGCAACATCAAGAGCGCAAGCGGCTTATCTTGAAGGAGATCTATC 300
OY 101 SerLeuLeuAArgCySerMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 301 TCGTTGCTCAGTGTGATGCGCCAAAGTCTTATTCGAACCGCGATTTTCGTTGGCATATT 360
OY 121 IleArgAsnGluLeuAlaAspGluGlnSerPheMetSerValAlaLysThrArgValLys 140
Db 361 ATTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGACGCGGCCAAGCAGAGATTAG 420
OY 141 GlnMetLeuAArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
Db 421 CAGATGTTACGCCCTCTGCAGGCTTCTTATTAACAAGATGGTTCACCTTGGAGG 480
OY 161 GluProArgLeuAArgProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 481 GAGCTCGGCTGAGGCGCATCTGGAAGGATCGATGATTCGATATGCCCTGCTATT 540
OY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 541 GCTACCCAGAACCGATCAACGCCCGATATGCTATTGCACTCGACGATATGAGAAAT 600
OY 201 LysLeuIleHisGlyIleAglIngnInPheLeuIleHisAlaArgArgGlnGlnLys 220
Db 601 AAATTGATTACGGTATCGCTCAGAGTTTCTTAATCCATGGCGCTGACAGAAACAGAA 660
OY 221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
Db 661 TTCCTTTGGTGGGCGGACAGCTGTGAAAGCGTTTGAAGCAACCATTTGGAATG 717
```

RESULT 3

US-10-817-483-1
; Sequence 1, Application US/10817483
; Publication No. US20040237147A1
; GENERAL INFORMATION:
; APPLICANT: Haben, Jeffrey E.
; APPLICANT: Zinsmeister, Christopher

APPLICANT: Tomes, Dwight
APPLICANT: Abbitc, Shane
APPLICANT: Helentjaris, Timothy G.
APPLICANT: Niu, Xiaomu
TITLE OF INVENTION: Modulation of cytokinin activity in
TITLE OF INVENTION: Plants
FILE REFERENCE: 0803R
CURRENT APPLICATION NUMBER: US/10/817,483
CURRENT FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: US 60/460,718
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 09/545,334
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/129,844
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1919
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
FEATURE:
NAME/KEY: CDS
LOCATION: (690)..(1411)
OTHER INFORMATION: 1pc
US-10-817-483-1

Alignment Scores:

Pred. No.: 1,57e-148 Length: 1919
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-817-483-2 (1-239) x US-10-817-483-1 (1-1919)

QY 1 MetApeLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 690 ATGATCTACGCTCTAATTTTCGGTCCAACTTCACAGAAAGACATCGACTCGATAGCT 749
QY 21 LeuIAGInGInThGlyLeuProValLeuSerLeuAspArgValGlnCysGlyProGln 40
DB 750 CTGGCCAGCAGACTGGCTCCCAAGTCTCTGCTCGATCGGCTCAATGCTGCTCTCA 809
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB 810 CTATCAACCGGAAGCGGCGGACCAACAGTGAAGAACTGAAGAAACGACTGCTGTGAC 869
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnuArgLeu 80
DB 870 CTGTATGATCGCCCTTTGGTAAAGGGTATCATTAACGCAAGCAAGCTCATGAAGCGCTC 929
QY 81 IleIAGIuValHisAsnHisGlnuAlaLysGlyLysLeuIleLeuGluGlySerIle 100
DB 930 ATTTGGAGGTGCAACATCAAGAGCCAAAGCGGCTTATCTTGAAGGAGATCTATC 989
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 990 TCGTTGCTCAGGTGCATGGCGCAAGTCTTATTTGGAACGCGGATTTTCTTGGCATATT 1049
QY 121 IleArgAsnGluLeuAlaAspGluLysSerPheMetSerValAlaLysThrArgValLys 140
DB 1050 ATTCACCAAGAGTTAGCAAGACAGAGAGCTTCATGAGCGTGGCCAAAGCCAGAGTTAAG 1109
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
DB 1110 CAGAGTTACGCCCTCTGCAAGTCTTTTATTAATCAAGAGTTGATCAACTTTGGAGG 1169
QY 161 GlnProArgLeuArgProIleLeuGluGlyLysAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB 1170 GAGCTCGGCTGAGGCCCATCTGGAAGGATCGATGATATGATATGCCCTGCTATT 1229

QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnIleAspAlaAspMetGlnuAsn 200
DB 1230 GCTACCCGGAACCAATATACGCCCTCATATGCTATGAGCTCGACGAGATATGAGAAAT 1289
QY 201 LysLeuIleHisGlyTleAlaGlnLupPheLeuIleHisAlaArgArgGlnGluLys 220
DB 1290 AAATTGATTCACGGATGCTGCTCAGAGATTTCATTCATTCGCGCTCGACAGAACAGAA 1349
QY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
DB 1350 TTCCCTTGTGGGGCGGACAGCTGTGAAAGGCTTTGAAGACCAATTTTGAATG 1406

RESULT 4

US-11-139-461-8
Sequence 8, Application US/11139461
Publication No. US20050229274A1
GENERAL INFORMATION:
APPLICANT: Zinselmeyer, Chris
APPLICANT: Haben, Jeff
TITLE OF INVENTION: Tomes, Dwight
TITLE OF INVENTION: Regulated Expression of Genes in Plant
FILE REFERENCE: 0803
CURRENT APPLICATION NUMBER: US/11/139,461
PRIOR FILING DATE: 2005-05-27
PRIOR APPLICATION NUMBER: US 60/129,844
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 2722
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter from Hordeum vulgare, Plant Journal 6:849-860
OTHER INFORMATION: (1994); gene from Agrobacterium tumefaciens, Molecular
OTHER INFORMATION: from Zea mays, Genbank Accession #S78780.
US-11-139-461-8

Alignment Scores:

Pred. No.: 2,6e-148 Length: 2722
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-817-483-2 (1-239) x US-11-139-461-8 (1-2722)

QY 1 MetApeLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
DB 1525 ATGATCTACGCTCTAATTTTCGGTCCAACTTCACAGAAAGACATCGACTCGATAGCT 1584
QY 21 LeuIAGInGInThGlyLeuProValLeuSerLeuAspArgValGlnCysGlyProGln 40
DB 1585 CTGGCCAGCAGACTGGCTCCCAAGTCTCTGCTCGATCGGCTCAATGCTGCTCTCA 1644
QY 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB 1645 CTATCAACCGGAAGCGGCGGACCAACAGTGAAGAACTGAAGAAACGACTGCTGTGAC 1704
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGlnuArgLeu 80
DB 1705 CTGTATGATCGCCCTTTGGTAAAGGTATCATTAACGCAAGCAAGCTCATGAAGCGCTC 1764
QY 81 IleIAGIuValHisAsnHisGlnuAlaLysGlyLysLeuIleLeuGluGlySerIle 100
DB 1765 ATTTGGAGGTGCAACATCAAGAGCCAAAGCGGCTTATCTTGAAGGAGATCTATC 1824
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB 1825 TCGTTGCTCAGGTGCATGGCGCAAGTCTTATTTGGAACGCGGATTTTCTTGGCATATT 1884

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OY 121 lIeaRgaNglUleuAlaAspGluGluSerPheMetSerValAlaIySThrArgVallys 140
DB 1885 ATTGCAACGAGTTAGACAGAGAGAGCTTCAATGAGCGGCGCAAGACCAAGATTAG 1944
OY 141 GluMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluValGlnLeuTrpArg 160
DB 1945 CAGATGTTACGCCCCCTCTGCGAGGTCTTTCTATTATTCAGAGGTTGGTTCACTTTGGAGG 2004
OY 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTrpArgTrpAlaLeuLeuPhe 180
DB 2005 GAGCCTGGCTGAGAGCCCATCTGGAAGGATCGATGATTCATATGCCCTCTATT 2064
OY 181 AlAthrgInbngInIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
DB 2065 GCTACCCAGAACCGATCACGCCCGATATGCTATTGCGCTCGACGCGAGATATGAGAA 2124
OY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGln 220
DB 2125 AAATTGATTACGGTATCGCTCAGAGAGTTTCTTAATTCATGCGCGCTCGACAGAAACAGAA 2184
OY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGlnGlyProProPheArgMet 239
DB 2185 TTCCTTTGGTGGCGGAGACAGCTGTGGAAGCGTTTGAAGACCAACATTTCGAATG 2241

RESULT 5
US-11-139-461-9
; Sequence 9, Application US/11139461
; Publication No. US20050229274A1
; GENERAL INFORMATION:
; APPLICANT: Zinsmeister, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/11/139,461
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/129,844
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Zea mays, U.S. patent application 09/377,648;
; OTHER INFORMATION: Gene from Agrobacterium tumefaciens, Molecular and General
; OTHER INFORMATION: Genetics 216:388-394 (1989); terminator from Solanum
; OTHER INFORMATION: tuberosum, Plant Cell 1(1):115-122 (1989).
US-11-139-461-9

Alignment Scores:
Pred. No.: 2,66-148 Length: 2722
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0

US-10-817-483-2 (1-239) x US-11-139-461-9 (1-2722)
OY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyIySThrSerThrAlaIleAla 20
DB 1525 ATGATCTACGCTTAATTTTGGTCCACACTGCACAGAAAGACATCGACTGCGATAGCT 1584
OY 21 LeuAlaGlnGlnInThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
DB 1585 CTTCCCAAGACAGACTGGCTCCAGTCTCTCGCTCGATCCGTCGAATGCTGTCCTCAA 1644
OY 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTrp 60
```

```
DB 1645 CTATCAACCGGAAGCGGGGCGACCAACAGTGGAGAACTGAAGAACAGACTCGTCTGAC 1704
OY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB 1705 CTTGATATCGCCCCCTTTGGTAAAGGCTATCATACACCAGCAAGCTCATGAAAGCGCTC 1764
OY 81 lIeAlaGluValHisAsnHisGluAlaLysGlyGlyLeuIleLeuGlnGlyIleSerIle 100
DB 1765 ATTGCGGAGGTGACCAATCACAGAGCCCAAGGCGGCTTATTTCTTGAGGAGGATCTATC 1824
OY 101 SerLeuLeuArgCysMetAlaGlnSerArgTrpTrpAsnAlaAspPheArgTrpHisIle 120
DB 1825 TCGTTGCTCAGGTCTCAGTGGCGCAAAAGCTTATTTGAAACGGGATTTTCGTTGCAATAT 1884
OY 121 lIeaRgaNglUleuAlaAspGluGluSerPheMetSerValAlaIySThrArgVallys 140
DB 1885 ATTGCAACGAGTTAGACAGAGAGCTTCAATGAGCGGCGCAAGACCAAGATTAG 1944
OY 141 GluMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluValGlnLeuTrpArg 160
DB 1945 CAGATGTTACGCCCCCTCTGCGAGGTCTTTCTATTATTCAGAGGTTGGTTCACTTTGGAGG 2004
OY 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyTrpArgTrpAlaLeuLeuPhe 180
DB 2005 GAGCCTGGCTGAGAGCCCATCTGGAAGGATCGATGATTCATATGCCCTCTATT 2064
OY 181 AlAthrgInbngInIleThrProAspMetLeuGlnLeuAspAlaAspMetGluAsn 200
DB 2065 GCTACCCAGAACCGATCACGCCCGATATGCTATTGCGCTCGACGCGAGATATGAGAA 2124
OY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGln 220
DB 2125 AAATTGATTACGGTATCGCTCAGAGAGTTTCTTAATTCATGCGCGCTCGACAGAAACAGAA 2184
OY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGlnGlyProProPheArgMet 239
DB 2185 TTCCTTTGGTGGCGGAGACAGCTGTGGAAGCGTTTGAAGACCAACATTTCGAATG 2241

RESULT 6
US-11-139-461-12
; Sequence 12, Application US/11139461
; Publication No. US20050229274A1
; GENERAL INFORMATION:
; APPLICANT: Zinsmeister, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/11/139,461
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/129,844
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 3017
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Zea mays, Genbank Accession #L22344;
; OTHER INFORMATION: Gene from Agrobacterium tumefaciens, Molecular and
; OTHER INFORMATION: General Genetics 216:388-394 (1989); terminator from
; OTHER INFORMATION: Zea mays, Genbank Accession #L22345.
US-11-139-461-12

Alignment Scores:
Pred. No.: 3,07e-148 Length: 3017
Score: 1230.00 Matches: 239
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 13 Gaps: 0
```


US-10-817-483-2 (1-239) x US-11-139-461-12 (1-3017)

```

OY      1 MetApeLeuAryLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleA 20
DB      1408 ATGATCTACGCTTAATTTTGGTCCAACTTGCACAGGAAAGACATCGACTCGATAGCT 1467
OY      21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGln 40
DB      1468 CTGGCCAGCAGACAGCTGGCTCCCAAGTCTCTGCTCGATCGGTCCTCAATGCTGCTCAA 1527
OY      41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB      1528 CTATACACCGAAGCGGCGGACCAACAGTGAAGAACTGAAGAAAGCACTGCTGTGAC 1587
OY      61 LeuAspApeAryProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB      1588 CTGATGATCGCCCTTTGGTAAAGGTATCATTTACAGCCAAAGCCTCATGACGGCTC 1647
OY      81 IleAlaGlnValHisAsnHisGluAlaLysGlyGlyLeuIleLeuGlnGlyLysSerIle 100
DB      1648 ATTCGGAGGTGCACAATCACAGAGCCAAAGCGGCTTATCTTGAGGAGAGATCTATC 1707
OY      101 SerLeuLeuAryCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB      1708 TCGTTGCTCAGGTGATGAGCGCAAGTCTTATTTGAAACGGGATTTTGTGGCATATT 1767
OY      121 IleArgAsnGlnLeuAlaAspGlnGluSerPheMetSerValAlaLysThrArgValLys 140
DB      1768 ATTGCACAGAGTTGACAGAGAGAGAGCTTCATGAGGCTGCGCAAGCCAGACTTAAAG 1827
OY      141 GlnMetLeuAryProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
DB      1828 CAGAGTTACCGCCCTCTGACAGTCTTCTATTATTCAAAGCTTGCTCAACTTGGAGG 1887
OY      161 GluProAryLeuAryProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB      1888 GAGCTCGGCTGAGGCGCCATCTGAGAGGATCGATGATTCGATATGCGCTGCTATTT 1947
OY      181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGlnAsn 200
DB      1948 GCTACCAAGAACCAATACAGCCGATATGCTATTGCAAGCTCGAAGCAGATATGAGAAAT 2007
OY      201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLys 220
DB      2008 AAATTGATTCAACGATATGCTGACAGAGTTTCTAATCCATGCGCTCGACAGGAACAGAAA 2067
OY      221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
DB      2068 TTCCCTTTGGTGGCGCGACAGCTGTGAAAGCGTTTGAAGACCAACCATTTGCAATG 2124

```

RESULT 7

```

; Sequence 7, Application US/11139461
; Publication No. US20050229274A1
; GENERAL INFORMATION:
; APPLICANT: Zinsmeister, Chris
; APPLICANT: Habben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/11/139,461
; PRIOR FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FASTSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 5622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

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; OTHER INFORMATION: Promoter and terminator from Zea mays as found in
; OTHER INFORMATION: Genbank Accession #S79780, gene from Agrobacterium
; OTHER INFORMATION: tumefaciens as found in Molecular and General
; OTHER INFORMATION: Genetics 216:388-394 (1989).
US-11-139-461-7

```

Alignment Scores:

| Pred. No.: | Length: | Matches: |
|------------------------|---------|-----------------|
| 7,42e-148 | 5622 | 239 |
| Score: | 1230.00 | |
| Percent Similarity: | 100.0% | Conservative: 0 |
| Best Local Similarity: | 100.0% | Mismatches: 0 |
| Query Match: | 100.0% | Indels: 0 |
| DB: | 13 | Gaps: 0 |

US-10-817-483-2 (1-239) x US-11-139-461-7 (1-5622)

```

OY      1 MetApeLeuAryLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleA 20
DB      1525 ATGATCTACGCTTAATTTTGGTCCAACTTGCACAGGAAAGACATCGACTCGATAGCT 1584
OY      21 LeuAlaGlnGlnThrGlyLeuProValIleuSerLeuAspArgValGlnCysCysProGln 40
DB      1585 CTGGCCAGCAGACTGGCTCCCAAGTCTCTGCTCGATCGGTCCTCAATGCTGCTCAA 1644
OY      41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
DB      1645 CTATACACCGAAGCGGCGGACCAACAGTGAAGAACTGAAGAAAGCACTGCTGTGAC 1704
OY      61 LeuAspApeAryProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
DB      1705 CTGATGATCGCCCTTTGGTAAAGGTATCATTTACAGCCAAAGCCTCATGACGGCTC 1764
OY      81 IleAlaGlnValHisAsnHisGluAlaLysGlyGlyLeuIleLeuGlnGlyLysSerIle 100
DB      1765 ATTCGGAGGTGCACAATCACAGAGCCAAAGCGGCTTATCTTGAGGAGATCTATC 1824
OY      101 SerLeuLeuAryCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
DB      1825 TCGTTGCTCAGGTGATGAGCGCAAGTCTTATTTGAAACGGGATTTTGTGGCATATT 1884
OY      121 IleArgAsnGlnLeuAlaAspGlnGluSerPheMetSerValAlaLysThrArgValLys 140
DB      1885 ATTGCACAGAGTTGACAGAGAGAGAGCTTCATGAGGCTGCGCAAGCCAGACTTAAAG 1944
OY      141 GlnMetLeuAryProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
DB      1945 CAGAGTTACCGCCCTCTGACAGTCTTCTATTATTCAAAGTTGCTTCAACTTGGAGG 2004
OY      161 GluProAryLeuAryProIleLeuGlnGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
DB      2005 GAGCTCGGCTGAGGCGCCATCTGAGAGGATCGATGATTCGATATGCGCTGCTATTT 2064
OY      181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGlnAsn 200
DB      2065 GCTACCAAGAACCAATACAGCCGATATGCTATTGCAAGCTCGAAGCAGATATGAGAAAT 2124
OY      201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnLys 220
DB      2125 AAATTGATTCAACGATATGCTGACAGAGTTTCTAATCCATGCGCTCGACAGGAACAGAAA 2184
OY      221 PheProLeuValGlyAlaThrAlaValGlnAlaPheGlnGlyProProPheArgMet 239
DB      2185 TTCCCTTTGGTGGCGCGACAGCTGTGAAAGCGTTTGAAGACCAACCATTTGCAATG 2241

```

RESULT 8

```

; Sequence 35042, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.

```

```

; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35042
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-35042

Alignment Scores:
Pred. No.: 5,47e-129 Length: 720
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
Gaps: 0
DB: 7

US-10-817-483-2 (1-239) x US-10-369-493-35042 (1-720)

Qy 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyYsthrSerThrAlaIleAla 20
Db 1 ATGATCTGCGCTAAATTTTGGTCCAACTTGCAAGAAAGACGTCCACCGCGTAGCT 60
Qy 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 61 CTGCGCCAGCAGACTGGGCTTCCAGTCTTCCGCTCGATCGGGTCCAAATGTTGCTCAG 120
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuYsglyYthrThrArgLeuYr 60
Db 121 CTGCAACCGGAAGCGAGCAGCAACAGTGGAGAAAGTGAAGAGACGCGCTATAC 180
Qy 61 LeuAspAspArgProLeuValIysGlyIleIleThrAlaIysGlnAlaIleGluArgLeu 80
Db 181 CTTATGATCGGCTCTGCTGTAAGGGTATCATCGACCAAGCAAGCTCATGAAGAAGCTG 240
Qy 81 IleAlaGlnValHisAsnHisGlnAlaIysGlyIleLeuGlnGlySerIle 100
Db 241 ATGGGGAGGTGTATATATATAGAGCCCAAGCGGCTTATTTGAGGAGATCTATC 300
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 301 TCGTTGCTCAAGTCGATGCGCAAGCAGTTATGAGTGCAGATTTTCGTTGGCATATT 360
Qy 121 IleArgAsnGlnLeuAlaAspGlnGlnSerPheMetSerValAlaIleThrArgValIys 140
Db 361 ATTGCCACGAGTTAGCAGACGAGAGAGCCTTCATGAACGTGGCCAAAGCCAGATTAA 420
Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
Db 421 CAGATGTTACCCCTGCTGCAAGGCTTCTATTAACAAGTGGTGGATCTTTGGA 480
Qy 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyYrArgYrAlaLeuLeuPhe 180
Db 481 GAGCCTCGGCTGAGGCGCATATCTGAAGAAGATCGATGATCGCATGCGATGTTT 540
Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGlnAsn 200
Db 541 GCTAGCCAGAAACCAATCATCATCCGATATGCTTATGAGCTTGAGAGCATATGAGAT 600
Qy 201 LysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHisAlaArgArgGlnGlnIys 220
Db 601 AAGTTGATTCATGGATGCTCTCAAGATATCTCATCCATGACGCGCAAGAACAGAAA 660
Qy 221 PheProLeuValGlyAlaIleThrAlaValAlaPheGlnGlyProProPheArgMet 239
Db 661 TTCCCTCGAGTTAACGACGCGCTTACGACGATTCGAAGGTTCATTCATTCGGAATG 717
```

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RESULT 9
US-10-369-493-38138
; Sequence 38138, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38138
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38138

Alignment Scores:
Pred. No.: 5,47e-129 Length: 720
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
Gaps: 0
DB: 7

US-10-817-483-2 (1-239) x US-10-369-493-38138 (1-720)

Qy 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyYsthrSerThrAlaIleAla 20
Db 1 ATGATCTGCGCTAAATTTTGGTCCAACTTGCAAGAAAGACGTCCACCGCGTAGCT 60
Qy 21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
Db 61 CTGCGCCAGCAGACTGGGCTTCCAGTCTTCCGCTCGATCGGGTCCAAATGTTGCTCAG 120
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGlnLeuYsglyYthrThrArgLeuYr 60
Db 121 CTGCAACCGGAAGCGAGCAGCAACAGTGGAGAAAGTGAAGAGACGCGCTATAC 180
Qy 61 LeuAspAspArgProLeuValIysGlyIleIleThrAlaIysGlnAlaIleGluArgLeu 80
Db 181 CTTATGATCGGCTCTGCTGTAAGGGTATCATCGACCAAGCAAGCTCATGAAGAAGCTG 240
Qy 81 IleAlaGlnValHisAsnHisGlnAlaIysGlyIleLeuGlnGlySerIle 100
Db 241 ATGGGGAGGTGTATATATATAGAGCCCAAGCGGCTTATTTGAGGAGATCTATC 300
Qy 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
Db 301 TCGTTGCTCAAGTCGATGCGCAAGCAGTTATGAGTGCAGATTTTCGTTGGCATATT 360
Qy 121 IleArgAsnGlnLeuAlaAspGlnGlnSerPheMetSerValAlaIleThrArgValIys 140
Db 361 ATTGCCACGAGTTAGCAGACGAGAGAGCCTTCATGAACGTGGCCAAAGCCAGATTAA 420
Qy 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArg 160
Db 421 CAGATGTTACCCCTGCTGCAAGGCTTCTATTAACAAGTGGTGGATCTTTGGA 480
Qy 161 GluProArgLeuArgProIleLeuGlnGlyIleAspGlyYrArgYrAlaLeuLeuPhe 180
Db 481 GAGCCTCGGCTGAGGCGCATATCTGAAGAAGATCGATGATCGCATGCGATGTTT 540
Qy 181 AlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAspMetGlnAsn 200
Db 541 GCTAGCCAGAAACCAATCATCATCCGATATGCTTATGAGCTTGAGAGCATATGAGAT 600
```

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Oy      201  yslsleuilehig1y1leaiaingluhpheleu1ehislaaragaingluindys 220
Db      601  AAGTTGATTCAATGGGATTCGCTCAGAGATATCTCATCATCACCACCAAGAACAGAA 660

Oy      221  phepPoleuValG1yAlaIathra1aValG1uAlaPhegluclgypProPheargMet 239
Db      661  TTCCCTCGAGTTAACCGCACCGCCGCTTCAGACGATTCGAAAGTCATTCATTCGAATG 717

RESULT 10
US-10-369-493-38549
Sequence 38549, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 38549
LENGTH: 720
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38549

Alignment Scores:
Pred. No.:      5,47e-129      Length:      720
Score:          1075.00      Matches:      206
Percent Similarity: 93.7%      Conservative: 18
Best Local Similarity: 86.2%      Mismatches:  15
Query Match:    87.4%      Indels:      0
DB:             7          Gaps:      0
US-10-817-483-2 (1-239) x US-10-369-493-38549 (1-720)

```

[illegible]

```

Db      421  CAGATGTTAGCGCCCTGTCAGAGCCTTTCTATTATCCAAAGAGTGTGATCTTTGGAAA 480
Qy      161  GlnProArlGleuArlArgProIleuGluGlyIleAspGlyTyrArgTyrAlaIleuIleuPhe 180
Db      481  GAACTCCGCGGTGGGGCCCATCTACTGAAAGATCGATGATGATATCGATATGCGCATGTGTGTT 540
Qy      181  AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGlnAsn 200
Db      541  GCTAGCCAGAACCATGATCATCTCCGATATGCTATTGGACGCTTGACGACGATATGGAGGAT 600
Qy      201  LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluGlnLys 220
Db      601  AAGTTGATTCATGAGGATCCGCTCAGAGGATTCATCATCCATGCGACGCCGACAGAACAGAAA 660
Qy      221  PheProLeuValGlyAlaThrAlaValAlaGluAlaPheGluGlyProProPheArgMet 239
Db      661  TTCCCTCGAGATTAAACGACGCCGCTTACGACGAGATTGGAAGTCATTCATTCGGAATG 717

RESULT 11
US-10-369-493-38954
; Sequence 38954, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianteng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38954
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; US-10-369-493-38954

```

| Alignment Scores: | | | |
|---|-----------|--|-----|
| Pred. No.: | 5,47e-129 | Length: | 720 |
| Score: | 1075.00 | Matches: | 206 |
| Percent Similarity: | 93.7% | Conservative: | 18 |
| Best Local Similarity: | 86.2% | Mismatches: | 15 |
| Query Match: | 87.4% | Indels: | 0 |
| DB: | 7 | Gaps: | 0 |
| US-10-817-483-2 (1-239) x US-10-369-493-38954 (1-720) | | | |
| QY | 1 | MetAspLeuArgLeuIleIlePheGlyProThrCysThrGlyValSerSerThrAlaIleAla | 20 |
| Dp | 1 | ATGGAGCTGGCGCTATATTTTCGGTCCAACTTGCAACAGAAAGAGCTGACCGCGTAGCT | 60 |
| QY | 21 | LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln | 40 |
| Dp | 61 | CTTGCCCAACAGACTGGGCTTCCAGTCTCTTCGCTCATCGGCTCCAAATGTTGCTCCAG | 120 |
| QY | 41 | LeuSerThrGlySerGlyArgProThrValGlnGlnLeuLeuGlyThrThrArgLeuTyr | 60 |
| Dp | 121 | CTGTCAACCGGAGCGGACGACCAACAGTGGAGAAACTGAAGAAGAAAGCAACCGCTATAC | 180 |
| QY | 61 | LeuAspAspArgProLeuValIleGlyLeuLeuThrAlaValGlnAlaHISGlnArgLeu | 80 |
| Dp | 181 | CTGTAGATGAGCGCTCTGTGTGAAGGTTTCATCCACGCAAGCAAGCTCAGTGAAGGCTG | 240 |
| QY | 81 | IleAlaGlnValAlaAsnHisGlnValAlaValGlyGlyLeuIleLeuGlnGlnGlySerIle | 100 |
| Dp | 241 | ATGGGAGGAGGTGTATTAATTATGAGGCCACGCGGGGCTTATTCTTGAAGGAGATCATC | 300 |
| QY | 101 | SerLeuLeuArgCysMetAlaGlnSerArgTyrTTrpAsnAlaAspPheAlaGlyTrpHisIle | 120 |

```
Db 301 TCGTTGCTCAAGTCATGCGCCAAAGCAGTTATTGAGTGGCGATTTTCGTTGGCATATT 360
Qy 121 IleaarganglualeuAaSPgluGluSerPheMetSerValAlaIyethrArgVallys 140
Db 361 ATTGGCCAGAGTTAGCAGACGAAAGACCTTCATGAACGTGGCCAAAGCCAGAGTTAAG 420
Qy 141 GlnMetLeuAargProSerAlaGlyLeuSerIleIleGlnGluValGlnLeuTrpArg 160
Db 421 CAGATGTTACGCCCTGCTGACGAGCCCTTCTATTATCCAAAGAGTTGGATTCTTTGGAAA 480
Qy 161 GluProAargLeuAargProIleIleGlnGluGlyIleAspGlyTrpArgTrpAlaLeuPhe 180
Db 481 GAGCTCGGCTGAGAGCCCATCTGAAAGAGATCCATGATATCCATATGCCATGTGTT 540
Qy 181 AlaThrGlnAengInIleThrProAspMetLeuGlnLeuAaSPAlaAspMetGluAsn 200
Db 541 GCTAGCCAGAACCGATCAGATCCGATATGCTATGACGCTTGACGAGATATGAGAGAT 600
Qy 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaIaArgGlnGlnGly 220
Db 601 AAGTTGATTATGAGGATCGCTCAGAGATATCTCATTCATGACGCCGCAAGAAACAGAAA 660
Qy 221 PheProLeuValGlyAlaIaThrAlaValaGluAlaPheGlnGlyProProPheArgMet 239
Db 661 TTCCTCGAGTTAACGACGCCGCTTACGACGATTCGAAAGTCATCCATTGCGAATG 717
```

```
RESULT 12
US-10-821-711-2
; Sequence 2, Application US/10821711
; Publication No. US20040237142A1
; GENERAL INFORMATION:
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Krieger, Elissa K
; APPLICANT: Ye, Xudong
; APPLICANT: Zhang, Mangsen
; TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF
; TITLE OF INVENTION: COMMERCIALLY VIABLE TRANSGENIC PLANTS
; FILE REFERENCE: 38-21(52967)B
; CURRENT APPLICATION NUMBER: US/10/821,711
; PRIORITY FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: 60/461,459
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 2
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-821-711-2
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Alignment Scores:
Pred. No.: 5,51e-129 Length: 723
Score: 1075.00 Matches: 206
Percent Similarity: 93.7% Conservative: 18
Best Local Similarity: 86.2% Mismatches: 15
Query Match: 87.4% Indels: 0
DB: 9 Gaps: 0
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US-10-817-483-2 (1-239) x US-10-821-711-2 (1-723)
Qy 1 MetAspLeuAargLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
Db 1 ATGATCTGCGCTTAATTTTGGGTCCAACTTGCACAGAAAGACGTCGACCCGGTAGCT 60
Qy 21 LeuAlaGlnInIthrGlyLeuProValLeuSerLeuAaSPArgValGlnCysCysProGln 40
Db 61 CTTGCCGAGACAGCTGGGCTTCCAGTCTTTCGCTCGATCGGATCCAAATGTTGCTCAG 120
Qy 41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuGlyGlyThrAlaGlnLeuTrp 60
Db 121 CTGTCAACCGGAGACGAGACCAACAGTGGAAAGAAAGGAAAGGACCGCTTATAC 180
Qy 61 LeuAspAaSPProLeuValGlyIleIleThrAlaLysGlnAlaHisGlyArgLeu 80
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Db 181 CTTATGATACGGCCTCTGCTGAAAGAGTATCATGCGACCCAGACGATCANTGAAGGCTG 240
Qy 81 IleaGluValHisAsnHisGlyAlaLysGlyLeuIleLeuGlnGlyIle 100
Db 241 ATGGGAGAGGTGTTAATTTATGAGGCCCGGCGGCTTATCTTGGAGGAGATCTATTC 300
Qy 101 SerLeuAargCysMetAlaGlnSerArgTrpTrpAsnAlaAaSPAaSPArgTrpHisIle 120
Db 301 TCGTTGCTCAAGTCATGCGCCAAAGCAGTTATTGAGTGGCGATTTTCGTTGGCATATT 360
Qy 121 IleaarganglualeuAaSPgluGluSerPheMetSerValAlaIyethrArgVallys 140
Db 361 ATTGGCCAGAGTTAGCAGACGAAAGACCTTCATGAACGTGGCCAAAGCCAGAGTTAAG 420
Qy 141 GlnMetLeuAargProSerAlaGlyLeuSerIleIleGlnGluValGlnLeuTrpArg 160
Db 421 CAGATGTTACGCCCTGCTGACGAGCCCTTCTATTATCCAAAGAGTTGGATTCTTTGGAAA 480
Qy 161 GluProAargLeuAargProIleIleGlnGluGlyIleAspGlyTrpArgTrpAlaLeuPhe 180
Db 481 GAGCTCGGCTGAGAGCCCATCTGAAAGAGATCCATGATATCCATATGCCATGTGTT 540
Qy 181 AlaThrGlnAengInIleThrProAspMetLeuGlnLeuAaSPAlaAspMetGluAsn 200
Db 541 GCTAGCCAGAACCGATCAGATCCGATATGCTATGACGCTTGACGAGATATGAGAGAT 600
Qy 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaIaArgGlnGlnGly 220
Db 601 AAGTTGATTATGAGGATCGCTCAGAGATATCTCATTCATGACGCCGCAAGAAACAGAAA 660
Qy 221 PheProLeuValGlyAlaIaThrAlaValaGluAlaPheGlnGlyProProPheArgMet 239
Db 661 TTCCTCGAGTTAACGACGCCGCTTACGACGATTCGAAAGTCATCCATTGCGAATG 717
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RESULT 13
US-11-156-084-1
; Sequence 1, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; TITLE OF INVENTION: agronomically interesting phenotypes
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; PRIORITY FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(723)
US-11-156-084-1
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Alignment Scores:
Pred. No.: 4,48e-128 Length: 723
Score: 1068.00 Matches: 205
Percent Similarity: 93.3% Conservative: 18
Best Local Similarity: 86.8% Mismatches: 16
Query Match: 86.8% Indels: 0
DB: 16 Gaps: 0
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US-10-817-483-2 (1-239) x US-11-156-084-1 (1-723)
Qy 1 MetAspLeuAargLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
Db 1 ATGATCTGCGCTTAATTTTGGGTCCAACTTGCACAGAAAGACGTCGACCCGGTAGCT 60
Qy 21 LeuAlaGlnInIthrGlyLeuProValLeuSerLeuAaSPArgValGlnCysCysProGln 40
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Db 61 CTGCCACAGACACCTGGCTTCCAGTCTTGGCTGCATCGGAGTCCAAATGTTCTCTCAG 120
QY 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyr 60
Db 121 CTGTCAACCGGAAGCGAGCAGCAACAGTGAAGAACTGAAGGAACGAGCCGTGATATC 180
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db 181 CTGTGATGATCGGCTCTGTGAAGGGTATCATCGCAGCCAAAGCTCATATAAAGGCTG 240
QY 81 IleAlaGluValHisAsnHisGlnAlaLysGlyLysGlyLeuIleLeuGluGlyGlySerIle 100
Db 241 ATGGGGGGGGGTATATATATATATAGAGCCAGCGCGGCTTATCTTGAGGAGAGATCTATC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTTPAsnAlaAspPheArgTTPHisIle 120
Db 301 TCGTTGCTCAAGTGCATGCGCCAAAGCAGTATTTGGAGTGGCGGATTTTCTTGCGCATAT 360
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
Db 361 ATTCGCCACGAGTTAGCAGACAGAAAGACCTTCATGAACGTGGCCAAAGCCAGAGTTAAG 420
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTTPArg 160
Db 421 CAGATGTTACGCTGCTGCTGAGGCTTTTATTTATTCAGAGTTGGTTGATCTTTGGAAA 480
QY 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 481 GAGCTCGGCTGAGGCGCCATCTGAAGAAGATCGATGATCGATATGCTCATTCGATGTTT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 541 GCTACCCAGAAACCAATCATCATCCATATGCTATGACCTTGACGCAATATGAGAGAT 600
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
Db 601 AAGTTGATTCATGGATGCTCAGAGATATCTCATTCATGTCAGCGCCAGAAAGAGAAA 660
QY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
Db 661 TTCCTCGAGTTAAGCGAGCGGCTTACAGCGATTCGAAGTTCATTCATTCGGAATG 717

RESULT 14

US-11-156-084-20
; Sequence 20, Application US/11156084
; Publication No. US2006010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (723)
US-11-156-084-20

Alignment Scores:

Pred. No.: 4 486-128 Length: 723
Score: 1068.00 Matches: 205
Percent Similarity: 93.3% Conservative: 18
Best Local Similarity: 85.8% Mismatches: 16
Query Match: 86.8% Indels: 0
DB: 16 Gaps: 0

US-10-817-483-2 (1-239) x US-11-156-084-20 (1-723)

QY 1 MetAspLeuArgLeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAla 20
Db 1 ATGATCTGGCGCTATATTTTCGCTCAACTGCAAGAGAAAGACTCGACCCCGGTAGTCT 60
QY 21 LeuAlaGlnIleThrGlyLeuProValLeuSerLeuAspArgValGlnCysProGln 40
Db 61 CTGCCACAGACACCTGGCTTCCAGTCTTGGCTGCATCGGAGTCCAAATGTTCTCTCAG 120
QY 41 LeuSerThrGlySerGlyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyr 60
Db 121 CTGTCAACCGGAAGCGAGCAGCAACAGTGAAGAACTGAAGGAACGAGCCGTGATATC 180
QY 61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
Db 181 CTGTGATGATCGGCTCTGTGAAGGGTATCATCGCAGCCAAAGCTCATATAAAGGCTG 240
QY 81 IleAlaGluValHisAsnHisGlnAlaLysGlyLysGlyLeuIleLeuGluGlyGlySerIle 100
Db 241 ATGGGGGGGGGTATATATATATATAGAGCCAGCGCGGCTTATCTTGAGGAGAGATCTATC 300
QY 101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTTPAsnAlaAspPheArgTTPHisIle 120
Db 301 TCGTTGCTCAAGTGCATGCGCCAAAGCAGTATTTGGAGTGGCGGATTTTCTTGCGCATAT 360
QY 121 IleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLys 140
Db 361 ATTCGCCACGAGTTAGCAGACAGAAAGACCTTCATGAACGTGGCCAAAGCCAGAGTTAAG 420
QY 141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTTPArg 160
Db 421 CAGATGTTACGCTGCTGCTGAGGCTTTTATTTATTCAGAGTTGGTTGATCTTTGGAAA 480
QY 161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
Db 481 GAGCTCGGCTGAGGCGCCATCTGAAGAAGATCGATGATCGATATGCTCATTCGATGTTT 540
QY 181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
Db 541 GCTACCCAGAAACCAATCATCATCCATATGCTATGACCTTGACGCAATATGAGAGAT 600
QY 201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
Db 601 AAGTTGATTCATGGATGCTCAGAGATATCTCATTCATGTCAGCGCCAGAAAGAGAAA 660
QY 221 PheProLeuValGlyAlaThrAlaValGluAlaPheGluGlyProProPheArgMet 239
Db 661 TTCCTCGAGTTAAGCGAGCGGCTTACAGCGATTCGAAGTTCATTCATTCGGAATG 717

RESULT 15

US-10-369-493-38969
; Sequence 38969, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38969
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens

US-10-369-493-38969

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 8.11e-128 | Length: | 720 |
| Score: | 1066.00 | Matches: | 205 |
| Percent Similarity: | 93.3% | Conservative: | 18 |
| Best Local Similarity: | 85.8% | Mismatches: | 16 |
| Query Match: | 86.7% | Indels: | 0 |
| DB: | 7 | Gaps: | 0 |

US-10-817-483-2 (1-239) x US-10-369-493-38969 (1-720)

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QY      21 LeuAlaGlnGlnThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGln 40
      61 CTTCGCCGACAGACTGGGCTTCCAGTCTTCGCTCGATCCGGTCCAAATGTTGCTCCAG 120
QY      41 LeuSerThrGlySerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyr 60
      121 CTGTCAACCGAAGGAGGAGACCAACACTGGAGAGACTGAAAGACGACCGCTTATAC 180
QY      61 LeuAspAspArgProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeu 80
      181 CTTGATGATCGGCTCTGTGTGAAGGATATCCAGCCCAAGCAAGTCATGAAAGGCTG 240
QY      81 IleAlaGluValHisAsnHisGluAlaLysGlyLeuIleLeuGluGlyGlySerIle 100
      241 ATGGGGGGGTGATTAATTATAGAGGCCCAAGCGGGCTTATCTTGAGGGAGATCTATC 300
QY      101 SerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIle 120
      301 TCGTTGCTCAAGTGCATGCGCCAAAGCACTTATGAGTGCAGATTTTCGTTGGATAT 360
QY      121 IleArgAsnGluLeuAlaAspGluGlnSerPheMetSerValAlaLysThrArgValLys 140
      361 ATTCGCCACGAGTTAGACGAGAGAGACTTTCATGAACGTGGCCAAAGCCAGAGTTAAG 420
QY      141 GlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArg 160
      421 CAGATGTTACCGCCCTGCTGCAGGCGCTTCTATTATCCAAAGAGTTGTTGATCTTGGAAA 480
QY      161 GluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLeuLeuPhe 180
      481 GAGCTTCGCTGAGGCCCATCTGAAAGAGATCGATGATATCCATATGCCATGTTGTTT 540
QY      181 AlaThrGlnAsnGlnIleThrProAspMetLeuLeuGlnLeuAspAlaAspMetGluAsn 200
      541 GCTAGCCGAAACAGATCACAATCCGATATGCTATTGCAGCTTGACGCGAGATATGAGGAT 600
QY      201 LysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGluLys 220
      601 AAGTTGATTCATGGATGCTCAGAGATATCTCATTCATGCAACGCCGCAAGAAACAGAAA 660
QY      221 PheProLeuValGlyAlaThrAlaValAlaGluAlaPheGluGlyProProPheArgMet 239
      661 TTCCTCGAGTTAAGCGACCGCTTACGACGAGATTGAAAGGTCATCCATTCGGAATG 717
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Search completed: June 26, 2006, 22:39:43
Job time : 1283 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 26, 2006, 20:38:53 ; Search time 38 Seconds
(without alignments)
2261.614 Million cell updates/sec

Title: US-10-817-483-2

Perfect score: 1230
Sequence: 1 MDLRIIFGPTCTGKTSTAIA.....KFLVGAATVAEAFSGPPPRM 239

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 296510 seqs, 119862409 residues

Total number of hits satisfying chosen parameters: 593020

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=published Applications_NA_New -OPMT=faetap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bitsum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-USER=US10817483 @GCN 1.1 30 @runat_26062006_142807_19093 -NCPU=6 -ICPU=3
-NO MMAP -NNG SCORES=0 -WAIT DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA_New.*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCR_NEW_PUB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 104.5 | 8.5 | 945 | US-10-471-571A-2309 | Sequence 2309, Ap |
| 2 | 83 | 6.7 | 2232 | US-11-217-529-81083 | Sequence 81083, A |
| 3 | 82.5 | 6.7 | 1011 | US-10-471-571A-2959 | Sequence 2959, Ap |
| 4 | 82.5 | 6.7 | 1501 | US-10-449-902-19636 | Sequence 19636, A |
| 5 | 82.5 | 6.7 | 2880 | US-10-449-902-19584 | Sequence 19584, A |
| 6 | 82 | 6.7 | 632 | US-10-953-349-25636 | Sequence 25636, A |
| 7 | 81.5 | 6.6 | 1798 | US-11-293-697-1637 | Sequence 1637, Ap |
| 8 | 81.5 | 6.6 | 2465 | US-10-449-902-10002 | Sequence 10002, A |
| 9 | 81.5 | 6.6 | 2989 | US-10-449-902-22349 | Sequence 22349, A |

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| 10 | 81.5 | 6.6 | 3243 | 7 | US-11-217-529-76988 | Sequence 76988, A |
| 11 | 81 | 6.6 | 651 | 6 | US-10-488-619-1211 | Sequence 1211, Ap |
| 12 | 81 | 6.6 | 659 | 6 | US-10-488-619-1209 | Sequence 1209, Ap |
| 13 | 81 | 6.6 | 1634 | 7 | US-11-293-697-1892 | Sequence 1892, Ap |
| 14 | 80.5 | 6.5 | 1061 | 6 | US-10-449-902-28331 | Sequence 28331, A |
| 15 | 80.5 | 6.5 | 2169 | 6 | US-10-449-902-18278 | Sequence 18278, A |
| 16 | 80.5 | 6.5 | 2511 | 6 | US-10-449-902-17618 | Sequence 17618, A |
| 17 | 80 | 6.5 | 1672 | 6 | US-10-449-902-20437 | Sequence 20437, A |
| 18 | 80 | 6.5 | 2353 | 6 | US-10-449-902-14983 | Sequence 14983, A |
| 19 | 79.5 | 6.5 | 1287 | 6 | US-10-449-902-14778 | Sequence 14778, Ap |
| 20 | 79.5 | 6.5 | 1377 | 6 | US-10-953-349-5460 | Sequence 5460, Ap |
| 21 | 79.5 | 6.5 | 1843 | 6 | US-10-449-902-4417 | Sequence 4417, Ap |
| 22 | 79.5 | 6.5 | 1974 | 6 | US-10-449-902-15620 | Sequence 15620, A |
| 23 | 79.5 | 6.5 | 2049 | 7 | US-11-217-529-79820 | Sequence 79820, A |
| 24 | 79 | 6.4 | 19634 | 6 | US-10-548-484-52 | Sequence 52, App1 |
| 25 | 79 | 6.4 | 13129 | 6 | US-10-517-441-84 | Sequence 84, App1 |
| 26 | 78.5 | 6.4 | 789 | 6 | US-10-471-571A-4555 | Sequence 4555, Ap |
| 27 | 78.5 | 6.4 | 1194 | 6 | US-10-471-571A-661 | Sequence 661, App |
| 28 | 78.5 | 6.4 | 1487 | 6 | US-10-449-902-22890 | Sequence 22890, A |
| 29 | 77.5 | 6.3 | 2017 | 6 | US-10-449-902-7616 | Sequence 7616, Ap |
| 30 | 77.5 | 6.3 | 2766 | 6 | US-10-449-902-24803 | Sequence 24803, A |
| 31 | 77 | 6.3 | 720 | 7 | US-11-217-529-2991 | Sequence 2991, Ap |
| 32 | 77 | 6.3 | 1629 | 6 | US-10-449-902-9909 | Sequence 9909, Ap |
| 33 | 77 | 6.3 | 3756 | 6 | US-10-449-902-12827 | Sequence 12827, A |
| 34 | 76.5 | 6.2 | 1023 | 7 | US-11-217-529-78199 | Sequence 78199, A |
| 35 | 76.5 | 6.2 | 1216 | 6 | US-10-449-902-21395 | Sequence 21395, A |
| 36 | 76.5 | 6.2 | 1638 | 7 | US-11-217-529-79683 | Sequence 79683, A |
| 37 | 76 | 6.2 | 709 | 6 | US-10-449-902-7541 | Sequence 7541, Ap |
| 38 | 76 | 6.2 | 795 | 7 | US-11-217-529-77108 | Sequence 77108, A |
| 39 | 76 | 6.2 | 1392 | 7 | US-11-217-529-516 | Sequence 516, App |
| 40 | 76 | 6.2 | 1637 | 6 | US-10-449-902-15922 | Sequence 15922, A |
| 41 | 76 | 6.2 | 1637 | 6 | US-10-449-902-22949 | Sequence 22949, A |
| 42 | 76 | 6.2 | 1723 | 6 | US-10-449-902-8091 | Sequence 8091, Ap |
| 43 | 75.5 | 6.1 | 1399 | 6 | US-10-449-902-11273 | Sequence 11273, A |
| 44 | 75.5 | 6.1 | 5040 | 7 | US-11-217-529-77055 | Sequence 77055, A |
| 45 | 75 | 6.1 | 1011 | 7 | US-11-217-529-80402 | Sequence 80402, A |

ALIGNMENTS

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RESULT 1
US-10-471-571A-2309
; Sequence 2309, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927MO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqMan199, version 1.03
; SEQ ID NO 2309
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-471-571A-2309

Alignment Scores:
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Score: 104.50 Matches: 57
Percent Similarity: 39.4% Conservative: 38
Best Local Similarity: 23.7% Mismatches: 63
Query Match: 8.5% Indels: 83
DB: Gaps: 12

US-10-817-483-2 (1-239) x US-10-471-571A-2309 (1-945)
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Db 40 GTAATTGGGGCCACATGCTTCAAGTAAACAGACGCTTTCAGATCAACTCGCAAGGCT 99
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Db      100 ATCAATGGTGAATCATTAAGCGGTGACTGATGCAAGCTCAAAACATATTAATTTGGA 159
Qy      45 SerGlyArgProThrValGlnGlnLeuLeuGlySerGlyThrArgLeuGlyTyrLeuAspArg 64
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Db      160 ACTGCAAAAGTAAACCTGAAAGAAATGAGTGTATTCCACATCATTTAATTTGAT----- 213
Qy      65 ProLeuValGlySerIleIleThrAla-----LysGln 75
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      214 -----ATCTGGAATCCGATGATACATTTTCAGCATATGAAATTCAGAGGA 258
Qy      76 AlaHisGluArgLeuIleAlaGluValHisAsnHisGluAlaGlySerGlyLeu---Ile 94
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      259 TTACAGAAAGATTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTC 309
Qy      95 LeuGlnGlySerIleSerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAla 114
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      310 ATAGCAGGTGGAACGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 345
Qy      115 AspPheArgTrpHisIleIleArgAsnGlnLeuAlaAspGlnGlnGlnSerPheMetSerVal 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      346 -----ATATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 372
Qy      135 AlaIysThrArgValGlySerGlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGln 154
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      373 -----ACAGTTACACCT---GCACAAATTAATTAATTAATTAATTAATTAATTAATTAAT 408
Qy      155 LeuValGlnLeuTrpArgGlnProArgLeuArgProIleLeuGlnGlyIleAspGlyTyr 174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      409 AAGTTAATCT-----GCATTAGAACATTAGAT----- 435
Qy      175 ArgTyrAlaLeuLeuPheAlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeu 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      436 -----AATCAGCACTACACAGATTATTAAGCTCAATTT 468
Qy      195 AspAla---AspMetGlnAsnLysLeuIleHisGlyIleAlaGlnGlnPheLeuIleHis 213
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      469 GATGGGTTTCTGCAGAAAT-----ATTCACTTAAACACCGCGCAAGAGTGTGGC 522
Qy      214 Ala-----ArgArgGlnGlnGlnGln 220
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      523 CCTATTGATATTATTATTAATAAACAATAAATTGTAATCGCAAGAAAGTCGAACAA 582
Qy      221 Phe 221
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      583 TTT 585

RESULT 2
US-11-217-529-81083
; Sequence 81083, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81083
; LENGTH: 2232
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81083
```

```
Alignment Scores:
Pred. No.: 3.27 Length: 2232
Score: 83.00 Matches: 46
Percent Similarity: 32.5% Conservative: 29
Best Local Similarity: 19.9% Mismatches: 72
Query Match: 6.7% Indels: 84
DB: 7 Gaps: 9

US-10-817-483-2 (1-239) x US-11-217-529-81083 (1-2232)
Qy      5 LeuIlePheGlyProThrCysThrGlyIleThrSerThrAlaIleAlaLeuAlaGlnGln 24
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      214 CTTATGTTTCATAGCAACCATTAACAGTAAATCTAAGTGGCCGACCGCATCCAAACAA 273
Qy      25 Thr----- 25
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      274 ACGGTTAACAAATATATGCTGTGATTTTTTTGCTTAATAATTAATTAATTAATTAATTC 333
Qy      26 -----GlyLeuProValLeuSerLeuArg-----ArgValGln 36
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      334 ATGACATCGATTCATCCGGTTATCCGATTGTAATGTAATGAGATTTTGCATTAAGC 393
Qy      37 CysCysProGlnLeuSerThrGlySerGlyArgProThrValGlnGlnLeuGlyThr 56
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      394 TCGGCTCTAGTATTTCACACATCTTCTAGATCATCGTTACGTTCTCTCTCTCTCTCTCTCTCT 450
Qy      57 ThrArgLeuTyrLeuAspAspArgProLeuValGlySerGlyIleIleThrAlaGlyGlnAla 76
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      451 -----AGGAGTTGAATGCTCAAGAACAAAGCT 477
Qy      77 HisGlnArgLeuIleAlaGlnValHisAsnHisGlnAlaGlySerGlyLeuIleLeuGln 96
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      478 CCCAAGCATTCATGCTAATGAACTAAGAAAG-----CTTTATCA 516
Qy      97 GlyIleSerIleSerLeu-----LeuArgCysMetAlaGlnSerArg--- 110
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      517 AATGATCTTTTACTACAGCAGCATTTGATTGATTAACTTGTACATGCAAAACGGGGA 576
Qy      111 -----TyrTrpAsnAlaAspPheArgTrpHis----- 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      577 TTCACGAAACACTCTTGAGTTTGATGATTTTGACCGGAGTTTATGTAAGAACTCGTT 636
Qy      120 -----IleIleArgAsnGlnLeuAla 126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      637 CTTATGACGAATCATCATACAGACAGACTAGATGTAACGCGCAAAAGAACTATTG 696
Qy      127 AspGlnGlnSerPheMetSerVal-----AlaIysThrArgValGln 141
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      697 GATCAACAGAGATTCTTCACGACCGTAATCCGAGGTTTGCTGAACAAATTTTAAGCTAT 756
Qy      142 MetLeuArgProSerAlaGlyLeuSerIleIleGlnGlnLeuValGlnLeuTrpArgGln 161
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      757 ATTAATAGTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 810
Qy      162 ProArgLeuArgProIleLeuGlnGlyIleAsp 172
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      811 GCAGGCACAAAGTTTAATGCAAGTGTATTAAT 843

RESULT 3
US-10-471-571A-2959
; Sequence 2959, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqMan99, version 1.03
```

SEQ ID NO 2959
LENGTH: 1011
TYPE: DNA
ORGANISM: Staphylococcus aureus
US-10-471-571A-2959

Alignment Scores:

| Pred. No.: | 1.24 | Length: | 1011 |
|------------------------|-------|---------------|------|
| Score: | 82.50 | Matches: | 49 |
| Percent Similarity: | 36.2% | Conservative: | 27 |
| Best Local Similarity: | 23.3% | Mismatches: | 67 |
| Query Match: | 6.7% | Indels: | 68 |
| DB: | 6 | Gaps: | 9 |

US-10-817-483-2 (1-239) x US-10-471-571A-2959 (1-1011)

```
OY 43 ThrGlySerGlyAArgProThrValGluGluLeuValGlyThrArgLeuThrLeuAsp 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 220 ACAGCTGAAGGTGAGCACTGATTCGCAATTGAAAGGTTACTTGCATATCTATGCAAGT 279
OY 63 AsparGProLeuValIleGlyIleIleThrAlaValGlnAlaHisGluArgLeuIleAla 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 280 GATTATCGTCTGTCAGAGGATTTAAGATAAATTTCAA-----ATTAG 324
OY 83 GluValHis-----AenHisGluAla----- 89
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 335 GAAGTTCATGTTGTTCTGCTGATGCTGATTAATGATCATCTGTAAACAGAAATTAGCT 384
OY 90 ---LysGlyGlyLeuIleLeuGluGly-----GlySerIleSerLeu-Le 103
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 385 AGACAAGCAGGTCATTACTTGAAGCATATTACAAAGAGCCGATGACTGCTGTACT 444
OY 103 uArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTyrHisIleIleArgAs 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 445 G-----GCGATCCAGATGGCAGTGTGA----- 469
OY 123 ngIuLeuAlaAspGluGluSerPheMetSerValAlaValThrArgValIleGluMetLe 143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 470 -----GTGMAACCAATTGCAT 483
OY 143 uArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGln-----Le 158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 484 TTATTATCCATTAATGATATTCTTCGATCCAGCAGAGGTGACTAGGCCAAATGTTGTC 543
OY 158 uTPArgGluProArgLeuArgProIleLeuGluGlyIleAspGlyTyrArgTyrAlaLe 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 544 TTTTCAGCAACACAACTTCACACCAAGTATGACCAACA--GCTGGCGGTATTATACGAC 602
OY 178 uLeuPheAlaThrGlnAsn-----GlnIleThrProAs 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 603 GATGATATGATCCTGATATGTCAGTAAACAACATATATACATTGTTGTAGACCCATC 662
OY 189 pMetLeuLeuGlnIleuAsp---AlaAspMetGluAsnGlySerIleHisGlyIleAlaG 208
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 663 AGTCATTAACACTTTATGACAAATTAACACACAAACGTTATATTACACGCAATTTGCTGA 722
OY 208 ngIuPheLeuIleHisAlaArgArgGln 217
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 723 TGCCTGAAGATGGCGCATCGACGTCAA 750
```

RESULT 4

US-10-449-902-19636
Sequence 19636, Application US/10449902
Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT DNA AND USRS THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449, 902
CURRENT FILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19636
LENGTH: 1501
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK069984
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-19636

Alignment Scores:

| Pred. No.: | 2.15 | Length: | 1501 |
|------------------------|-------------------------------------|---------------|------|
| Score: | 82.50 <td>Matches:</td> <td>59</td> | Matches: | 59 |
| Percent Similarity: | 36.8% | Conservative: | 44 |
| Best Local Similarity: | 21.1% | Mismatches: | 74 |
| Query Match: | 6.7% | Indels: | 104 |
| DB: | 6 | Gaps: | 11 |

US-10-817-483-2 (1-239) x US-10-449-902-19636 (1-1501)

```
OY 5 LeuIlePheGlyProThrCysThrGlyIleThrSerThrAlaIleAlaLeuAlaGln--- 23
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 352 TTGCTTATGAGCCTCCGCGCAGTGGAAACATGACAAATACCTGCGTTCAGAGAAAG 411
OY 24 -----GlnThrGly 26
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 412 TTGTATGGGTCACTATGCAACATGATTTCTTAATCTCATGATCATGATAGAGGTGCT 471
OY 27 LeuProValLeu-----SerLeuAspArgValGlnCysCysProGln-LeuSerThrG 44
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 472 ATTGATGTGTGAAGCAGCAAAATCCA-AGACTTCGCAAGTGCAGCCGACGCTCTCTTTCGG 530
OY 44 ySerGly----- 46
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 531 AGCAAGAACATCTGTTAAGATGTTCTATTGATGAGAACAGATGCCATGACCAAGATGC 590
OY 47 -----ArgProThrValGluGluLeuIleGlyThrThrArgLeuThrLeuAs 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 591 ACAATTGTCATTCGCAAGAGTCATTGAGAACATACAAAGAGCAAGAGTTTGCCTGAT 650
OY 62 pAspArgProLeuValIleGlyIleIleThrAlaValGlnAla----- 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 651 ATGCAACCATGTGAACAAH---ATCATTCACAGACTGCATACAGAGTGCACCAAGTTAG 707
OY 77 -----HisGluArgLeuIleAlaGluValHisAsnHis 87
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 708 ATTGCACCCCTTGATGCACTCATGTATGAGGAAGCTCTT-----AAACATATAAT 758
OY 87 sGluAlaIleGlyLeuIleLeuGluGlySerIleSerLeuLeuArgCysMetAl 107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 759 ACAATCCAGAGGCTTGATGATGATGACGAGGTTTGAACGCTTGGCGGTAAAGT-- 816
OY 107 aGlnSerArgTyrTrpAsnAlaAspPheArg-----TrpHis 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 817 -----AATGCTGATATGAGAGAGAGCTTTGAACATATTGCACTACACACA 860
OY 119 sIleIleArgAsnGluLeuAlaAspGluGluSerPheMetSerValAlaValThrArgVa 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 861 CATGCACTTAAGCAAAATTAACAGAGAGCTGTGATCCTTGACACAGAAACCCCATGCC 920
OY 139 lIleGlnMetLeuArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTr 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 921 GAAAGACATY-----GAAACAGATGACATCTAG 947
OY 159 P-----ArgGluProArgLeuArgPr 166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 948 GTTCTGAATGATTCATTTTCAACACAGCTTCAATATGATATATGAAAGATGAGAAA 1007
```


| | | | | |
|---|--|---|--|------|
| Oy | | 60 | TyrLeuaApAparXProLeuValylsglyleIeThraAlayGlnlAhiegluArg | 79 |
| Db | | 100 | TCCTTGATTTGGACCTCTATCTCTTATGTAGACTTTGCATTCAAAAGAACA----- | 50 |
| Oy | | 80 | LeuilealagluvalHieAsnHieglualaylsglylyLeuIlleuglu | 96 |
| Db | | 49 | -----GTTGGCGTGAATGAAAAACGAACCAATGTAGTCAAAATGTTGAA | 5 |
| RESULT 7 | | | | |
| | US-11-293-697-1637 | | | |
| | ; Sequence 1637, Application US/11293697 | | | |
| | ; Publication No. US20060105376A1 | | | |
| | ; GENERAL INFORMATION: | | | |
| | ; APPLICANT: HELIX RESEARCH INSTITUTE | | | |
| | ; TITLE OF INVENTION: Novel full length cDNA | | | |
| | ; FILE REFERENCE: H1-A0106 | | | |
| | ; CURRENT APPLICATION NUMBER: US/11/293,697 | | | |
| | ; CURRENT FILING DATE: 2005-12-05 | | | |
| | ; PRIOR APPLICATION NUMBER: US/10/108,260 | | | |
| | ; PRIOR FILING DATE: 2002-03-28 | | | |
| | ; NUMBER OF SEQ ID NOS: 5458 | | | |
| | ; SOFTWARE: PatentIn Ver. 2.1 | | | |
| | ; SEQ ID NO 1637 | | | |
| | ; LENGTH: 1798 | | | |
| | ; TYPE: DNA | | | |
| | ; ORGANISM: Homo sapiens | | | |
| | US-11-293-697-1637 | | | |
| Alignment Scores: | | | | |
| Pred. No.: | 3.61 | Length: | 1798 | |
| Score: | 81.50 | Matches: | 54 | |
| Percent Similarity: | 39.14 | Conservative: | 42 | |
| Best Local Similarity: | 21.84 | Mismatches: | 83 | |
| Query Match: | 6.64 | Indels: | 69 | |
| Db: | 7 | Gaps: | 11 | |
| US-10-817-483-2 (1-239) x US-11-293-697-1637 (1-1798) | | | | |
| Oy | 21 | LeuilaGlnlInThrGlyLeu----- | Provallenseurleuasp | 33 |
| Db | 659 | CTTGCCCGAGAGAAATCCATAGAGAAAGTGTCTTAGAAAACCATTTCAGAGCTGCAC | | 718 |
| Oy | 34 | ArgValGlnCywCysProGlnDeuserThrglySerGlyArgProThrValGlulueu | | 53 |
| Db | 719 | AGACTTGAG----- | CAAAAACAG | 736 |
| Oy | 54 | LysGlyThrThrArgLeuTyrlenuaspaParProLeuValylsGlylleleThrala | | 73 |
| Db | 737 | AAAGAAACCTACCCGCCGCGCATGCTAGACAG----- | CTGTTGCTGCC | 778 |
| Oy | 74 | LysGlnAlahiegluArgLeuilealaglivalHieasnHieglualaIylsgly----- | | 91 |
| Db | 779 | GAGAAAGTGCATAGGCGCACCCGTATACAGATTAGAGAAACGAGAACATTAACACACTGAC | | 838 |
| Oy | 92 | -----GlyleuileugluglylglySeriIeserleuenu | | 103 |
| Db | 839 | TACATGACAAGAGCGACGACTTACCAACCGTGTGAGACGAGGACGGAGAGGTTATAA | | 898 |
| Oy | 104 | ArgCysMetAlaGlnserHargTrYrrTpshala----- | Asphearg | 117 |
| Db | 899 | AAGCTCCCTTGAAACAAGAAAGGCTTATACAGCCCGCAAAGAAAGAAATGCTTAACGA | | 958 |
| Oy | 118 | TrpHisIleIleArgAsnglubeulaIspergJugluserePhemetSerValAlaysthr | | 137 |
| Db | 959 | CTCATTAACATPAAGAGATGAGCTTGTAACTCAATCTTT---GCACTCATGCTGGNG | | 1015 |
| Oy | 138 | ArgValIylsGlnMetLeuArgProSerAlaglyleuserIle-----IleGlnclueu | | 155 |
| Db | 1016 | GATGAAGAACAAATCCACATGTGAACAACTTGGCTGCAAGCCAAAGATACAGCATCTT | | 1075 |
| Oy | 156 | ValGlnleutPARG-----GluProArgLeuArgProIleleuGluluglylleasply | | 173 |

| | | | |
|---|--|---|-------|
| Db | 1076 | ACTCAGAAAGCTGAGGGAAGAAAGAGAGAGCTCAAAAGCATT----- | 11117 |
| Oy | 174 | TyrAtrgYrAlaLeuLeuPheAlaThrGlnAsnGlnIleThrProAspMetLeuLeuGln | 193 |
| Db | 1118 | -----ACCTCCAAATCCCAAMAGACAGACAGAAATTGCTCAGG | 1156 |
| Oy | 194 | LeuAspAlaAspMetGluAsnLysLeuIleHisIsglyIleAlaGlnGluPheLeuIleHis | 213 |
| Db | 1157 | TTAAAGTGGGCTTTGGTAACACAGAGCTTCGAGGTTTCTCAAGAGCATGAAGAGATGAAC | 1216 |
| Oy | 214 | AlaArgArgGlnGlnGlu-----LysPheProLeuValGlyAla | 226 |
| Db | 1217 | GCTAAAGCTGGCTATCAAGAGTCTCAGATATAGCAACTTATGACTCAAGCTGCTGGCTTA | 1276 |
| Oy | 227 | Thr---AlaValGluAlaPheGlu | 233 |
| Db | 1277 | ACCCAAAGAAATCGAGGAGCTAGAA | 1300 |
| RESULT 8 | | | |
| US-10-449-902-10002 | Sequence 10002, Application US/104499902 | | |
| Publication No. US20060123505A1 | GENERAL INFORMATION: | | |
| APPLICANT: National Institute of Agrobiological Sciences. | APPLICANT: Bio-oriented Technology Research Advancement Institution. | | |
| APPLICANT: The Institute of Physical and Chemical Research. | APPLICANT: Foundation for Advancement of International Science. | | |
| TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF | FILE REFERENCE: MOA-A0205Y1-US | | |
| CURRENT APPLICATION NUMBER: US/10/449, 902 | CURRENT FILING DATE: 2003-05-29 | | |
| PRIOR APPLICATION NUMBER: JP 2002-203369 | PRIOR FILING DATE: 2002-05-30 | | |
| PRIOR APPLICATION NUMBER: JP 2002-383870 | PRIOR FILING DATE: 2002-12-11 | | |
| NUMBER OF SEQ ID NOS: 56791 | SOFTWARE: PatentIn Ver. 2.1 | | |
| SEQ ID NO 10002 | LENGTH: 2465 | | |
| TYPE: DNA | ORGANISM: Oryza sativa | | |
| PUBLICATION INFORMATION: | DATABASE ACCESSION NUMBER: AK107350 | | |
| DATABASE ENTRY DATE: 2002-08-28 | US-10-449-902-10002 | | |
| Alignment Scores: | | | |
| Pred. No.: | 5.61 | Length: | 2465 |
| Score: | 81.50 | Matches: | 41 |
| Percent Similarity: | 34.1% | Conservative: | 17 |
| Best Local Similarity: | 24.1% | Mismatches: | 38 |
| Query Match: | 6.6% | Indels: | 75 |
| DB: | 6 | Gaps: | 6 |
| US-10-817-483-2 (1-239) x US-10-449-902-10002 (1-2465) | | | |
| Oy | 5 | LeuIlePheGlyProThrCysThrGlyLysThrSerThrAlaIleAlaLeuAlaGlnGln | 24 |
| Db | 1740 | TTGTTGTTTCGGGGCCACGGGAAACAGAGGAAACATGCTGCAAAGGCTATAGCCAAATGAC | 1799 |
| Oy | 25 | ThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSerThrGly | 44 |
| Db | 1800 | GCTGGTG--CCAGCTTCATCAATGTCCTGA-----GTCACCACTATCAATCGAAGTGT | 1851 |
| Oy | 45 | SerGlyArgProThrValGlnGluLeuLysGlyThrThrArgLeuTyrLeuAspAspArg | 64 |
| Db | 1852 | TCGGGGAGG----- | 1860 |
| Oy | 65 | ProLeuValLysGlyIleIleThrAlaLysGlnAlaHisGluArgLeuIleAlaGluVal | 84 |
| Db | 1861 | -----ACGAGAAAAACGTC----- | 1875 |
| Oy | 85 | HisAsnHisGluAlaLysGlyGlyLeuIleLeuGlnGluTylGlySerIleSerLeuLeuArg | 104 |

```
Db 1876 -----GAGCATGTCAGTTGGCTGCTAAG 1902
Qy 105 CysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIleIle----- 121
Db 1903 TTGCTCCTACATCATTTTGTG-----ATGAGGTGACAGTATGTAGACAGC 1953
Qy 122 -----ArgAsnGluLeuAlaAspGluGluSer 130
Db 1954 GCGCTCGATGCGGTGAACATGAGCGATGCGGAAGATCAAGAAATGATTGAGTCACT 2013
Qy 131 PheMetSerValAlaIleThrArgValIleGln----- 141
Db 2014 GGGATGGCTCTCTGCAAAATCGGGTGAAGAAATCCTTGTCTTGCTCTCAAAATAGAC 2073
Qy 142 -----MetLeuArgProSerAlaGly 148
Db 2074 CCTTGAATCTTGATGAAGCATCATTTAGGA 2103

RESULT 9
US-10-449-902-22349
; Sequence 22349, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22349
; LENGTH: 2989
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK072537
; DATABASE ENTRY DATE: 2001-12-06
; US-10-449-902-22349

Alignment Scores:
Pred. No.: 7.34 Length: 2989
Score: 81.50 Matches: 41
Percent Similarity: 34.1% Conservative: 17
Best Local Similarity: 24.1% Mismatches: 38
Query Match: 6.6% Indels: 75
Gaps: 6

US-10-817-483-2 (1-239) x US-10-449-902-22349 (1-2989)
Qy 5 LeuIlePheGlyProThrCysThrGlyThrSerThrAlaIleAlaLeuAlaGln 24
Db 1741 TTGTTGTTGGGGCCACCGGAAACAGGGAAACAATGCTTGCAAAAGGCTATGCGCAATGAC 1800
Qy 25 ThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSerThrGly 44
Db 1801 GCTGGTG--CCAGCTTCATCAATGCTCTGA-----TGTCCACCATCAATCAAGAGTGGT 1852
Qy 45 SerGlyArgProThrValGluGluLeuLeuSerGlyThrThrArgLeuTyLeuAspArg 64
Db 1853 TCGGGGAG----- 1861
Qy 65 ProLeuValIleGlyIleIleThrAlaIleGlnAlaHisGluArgLeuIleAlaGluVal 84
Db 1862 -----ACGAGAAAACGTCC----- 1876
```

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Qy 85 HisAsnHisGluAlaIleGlyGlyLeuIleLeuGluGlyGlySerIleSerLeuLeuArg 104
Db 1877 -----GAGCATGTCAGTTGGCTGCTAAG 1903
Qy 105 CysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIleIle----- 121
Db 1904 TTGCTCCTACATCATTTTGTG-----ATGAGGTGACAGTATGTAGACAGC 1954
Qy 122 -----ArgAsnGluLeuAlaAspGluGluSer 130
Db 1955 GCGCTCGATGCGGTGAACATGAGCGATGCGGAAGATCAAGAAATGATTGAGTCACT 2014
Qy 131 PheMetSerValAlaIleThrArgValIleGln----- 141
Db 2015 GGGATGGCTCTCTGCAAAATCGGGTGAAGAAATCCTTGTCTTGCTCTCAAAATAGAC 2074
Qy 142 -----MetLeuArgProSerAlaGly 148
Db 2075 CCTTGAATCTTGATGAAGCATCATTTAGGA 2104

RESULT 10
US-11-217-529-76988
; Sequence 76988, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO LIMITED
; APPLICANT: NAKAO, YOSHIIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217, 529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76988
; LENGTH: 3243
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-76988

Alignment Scores:
Pred. No.: 8.22 Length: 3243
Score: 81.50 Matches: 26
Percent Similarity: 41.3% Conservative: 12
Best Local Similarity: 28.3% Mismatches: 43
Query Match: 6.6% Indels: 11
Gaps: 2

US-10-817-483-2 (1-239) x US-11-217-529-76988 (1-3243)
Qy 55 GlyThrThrArgLeuTyTrpLeuAspArgProLeuValIleGlyIleIleThrAlaIle 74
Db 166 GGTACAAAGCGACCTATATATGATGACGATCGCCCAATGTTAAACAATGCAAGTACGCGA 225
Qy 75 GlnAlaHisGluArgLeuIleAlaGluValHisAsnHisGluAlaIleGlyGlyLeuIle 94
Db 226 CAGTACAT-----GCTACTTAACAACAGCCAAAGCGCCCATATGTA 267
Qy 95 LeuGluGlyGlySerIleSerLeuLeuArgCysMetAlaGlnSerArgTyrTrpAsnAla 114
Db 268 AATAAAGAAATGCAATCAATGATGCGGAGCGCATGCTCTCAATCAACGATATTCAAATAGC 327
Qy 115 AspPheArgTrpHisIleIleArgAsnGluLeuAlaAspGluGluSerPheMetSerVal 134
Db 328 AAT-----GTTCACAAATACATTAGCGTCTTGAGTGGATGATCTCTTCCACA 372
Qy 135 AlaIleThrArgValIleGlnMetLeuArgProSer 146
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Db 373 GAATCTGCTCTGCTTTTGGACAAGACCACTTCA 408

RESULT 11

US-10-488-619-1211

Sequence 1211, Application US//10488619

Publication No. US20060099578A1

GENERAL INFORMATION:

APPLICANT: Greenlee, Winner and Sullivan, P.C.

TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations

FILE REFERENCE: 98-01 WO

CURRENT APPLICATION NUMBER: US/10/488,619

CURRENT FILING DATE: 2004-03-01

NUMBER OF SEQ ID NOS: 3040

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1211

LENGTH: 651

TYPE: DNA

ORGANISM: Mus musculus

US-10-488-619-1211

Alignment Scores:

| Pred. No.: | 1 | Length: | 651 |
|------------------------|-------|---------------|-----|
| Score: | 81.00 | Matches: | 31 |
| Percent Similarity: | 41.2% | Conservative: | 18 |
| Best Local Similarity: | 26.1% | Mismatches: | 49 |
| Query Match: | 6.6% | Indels: | 21 |
| DB: | 6 | Gaps: | 3 |

US-10-817-483-2 (1-239) x US-10-488-619-1211 (1-651)

QY 5 LeuilepneglyprothChyethrlylyserThrAlaileAlaLeuAlaGln 24

Db 54 CTGCTCTGAGGACCCCGACGACCTGGAGACATTTGTTGCCGCTGTGCATCAT 113

QY 25 ThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSerThrgly 44

Db 114 ACAGACTGACTCTTATTTCGTGTC----- 137

QY 45 SerGlyArgProThrValGlnGlnLeuLeuysglyThrThrArgLeuTyrlLeuAspArg 64

Db 138 TCTGCTCTGAACTGTACAGAAATTCATCGG-----GAAGGGCA 179

QY 65 ProLeuValLySGlyIleleThrAlaLySGlnAlaHISGluArgLeuIleAlaGlnVal 84

Db 180 AGAATGTGAGGAGACTGTTGTCTATGCGCCGAGAACTGCTCCATCATCTTCATG 239

QY 85 HisAsnHisGlnAlaLySGlyIleLeuLeuGlnGlnGlySer-IleSerLeuLeuArg 104

Db 240 GACGAGATTGACTCTATTGCTCTCCACGCGCTGGAGGGGGCTCTGAGGCGACAGTGAG 299

QY 104 GCysMetAlaGlnSerArgTyrlTrpAsnAlaAspArgTrpHisIleLeuArg 122

Db 300 GTACAGCGCA-----CGATCTGGAATCTCTCATCATGCTGATGGCTTTGAGG 348

RESULT 12

US-10-488-619-1209

Sequence 1209, Application US//10488619

Publication No. US20060099578A1

GENERAL INFORMATION:

APPLICANT: Greenlee, Winner and Sullivan, P.C.

TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations

FILE REFERENCE: 98-01 WO

CURRENT APPLICATION NUMBER: US/10/488,619

CURRENT FILING DATE: 2004-03-01

NUMBER OF SEQ ID NOS: 3040

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1209

LENGTH: 659

TYPE: DNA

ORGANISM: Mus musculus

US-10-488-619-1209

Alignment Scores:

| Pred. No.: | 1.02 | Length: | 659 |
|------------------------|-------|---------------|-----|
| Score: | 81.00 | Matches: | 31 |
| Percent Similarity: | 41.2% | Conservative: | 18 |
| Best Local Similarity: | 26.1% | Mismatches: | 49 |
| Query Match: | 6.6% | Indels: | 21 |
| DB: | 6 | Gaps: | 3 |

US-10-817-483-2 (1-239) x US-10-488-619-1209 (1-659)

QY 5 LeuilepneglyprothChyethrlylyserThrAlaileAlaLeuAlaGln 24

Db 54 CTGCTCTGAGGACCCCGACGACCTGGAGACATTTGTTGCCGCTGTGCATCAT 113

QY 25 ThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSerThrgly 44

Db 114 ACAGACTGACTCTTATTTCGTGTC----- 137

QY 45 SerGlyArgProThrValGlnGlnLeuLeuysglyThrThrArgLeuTyrlLeuAspArg 64

Db 138 TCTGCTCTGAACTGTACAGAAATTCATCGG-----GAAGGGCA 179

QY 65 ProLeuValLySGlyIleleThrAlaLySGlnAlaHISGluArgLeuIleAlaGlnVal 84

Db 180 AGAATGTGAGGAGACTGTTGTCTATGCGCCGAGAACTGCTCCATCATCTTCATG 239

QY 85 HisAsnHisGlnAlaLySGlyIleLeuLeuGlnGlnGlySer-IleSerLeuLeuArg 104

Db 240 GACGAGATTGACTCTATTGCTCTCCACGCGCTGGAGGGGGCTCTGAGGCGACAGTGAG 299

QY 104 GCysMetAlaGlnSerArgTyrlTrpAsnAlaAspArgTrpHisIleLeuArg 122

Db 300 GTACAGCGCA-----CGATCTGGAATCTCTCATCATGCTGATGGCTTTGAGG 348

RESULT 13

US-11-293-697-1892

Sequence 1892, Application US//11293697

Publication No. US20060105376A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: Novel full length cDNA

FILE REFERENCE: HI-A0106

CURRENT APPLICATION NUMBER: US/11/293,697

CURRENT FILING DATE: 2005-12-05

PRIOR APPLICATION NUMBER: US/10/108,260

PRIOR FILING DATE: 2002-03-28

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1892

LENGTH: 1634

TYPE: DNA

ORGANISM: Homo sapiens

US-11-293-697-1892

Alignment Scores:

| Pred. No.: | 3.62 | Length: | 1634 |
|------------------------|-------|---------------|------|
| Score: | 81.00 | Matches: | 55 |
| Percent Similarity: | 36.5% | Conservative: | 44 |
| Best Local Similarity: | 20.3% | Mismatches: | 96 |
| Query Match: | 6.6% | Indels: | 76 |
| DB: | 7 | Gaps: | 10 |

US-10-817-483-2 (1-239) x US-11-293-697-1892 (1-1634)

QY 5 LeuilepneglyprothChyethrlylyserThrAlaileAlaLeuAlaGln 24

Db 834 CTGATGTTGAGACCCCGACGACCTGTAAACTATGCTAGTAAGCTGTGCACTGAA 893

QY 25 ThrGlyLeuProValLeuSerLeuAspArgValGlnCysCysProGlnLeuSerThrgly 44

Db 894 TGTGTACAACATTTCTCAACGTTTCG-----CCTTACACTGACACTCT 938

Qy 45 SerGlyArgProThrValGluGluLeu-----Lys 54
Db 939 AAMATACAGAGGTGAATCTGAGAGGTAGTTCGTGTTGTTGAGATGGCTAGATTTTAT 998
Qy 55 GLyThrArgValLeuAspArgProLeuVal-----LysGlyIleIle 71
Db 999 GCCCTTACACAGATCTTCATTTGATGAGATATCTATCTGACATCCAGAGGAACTCT 1058
Qy 72 ThrAlaLeuGlnAlaHisGluArgLeuIleAlaGlu--ValHisAsnHisGluAlaLys 90
Db 1059 GATGACATGAGCAGAGTCCAGAGGTCAAGTCTGAACCTCATTCAGATGATGATGAGT 1118
Qy 91 GLyGlyLeuIleLeuGluGlyGlySerLeuSerLeuAspGlySerMetAlaGlnSerArg 110
Db 1119 GGAGGAGCTTTGAAATGATGATCTTCACAAATGGTTATGATGATGAGTCTGCTACT-- 1175
Qy 111 TyrTrpAsnAlaAspPheArgTrpHisIleIleArgAsnGluLeuAlaAspGluGlySer 130
Db 1176 -----AATTTCCCGTGGGACAT-----GATGAGCT 1202
Qy 131 PheMetSerValAlaValThrArgValLeuGlnMetLeuArgProSerAlaGly----- 148
Db 1203 TTGCGAAGAAAGTTGAAAGGATATATATACCTCTCCACAGACGAAAGGAAAGCT 1262
Qy 149 -----LeuSerIleIleGlnGluLeuValGlnLeuTrpArgGluProArgLeuArgPro 166
Db 1263 GAGCTTCTGAAGATCAACCTTCGTGAGGTGCAATTTAGATCTGTATTTCAACTGGAAGAT 1322
Qy 167 IleLeuGluGlyIleAspGlyTyr-----ArgTyrAla 177
Db 1323 ATACCCAGAAAGATTTGAGGCGTATTCGTGCTGACATCACTAATGTTTGAGAGGATGCC 1382
Qy 178 LeuLeuPheAlaThrGlnAsnGlnIleThrProAspMetLeuGlnLeuAspAlaAsp 197
Db 1383 TCTTAAATGGCAATGACAGCGCGCT----- 1406
Qy 198 MetGluAsnLysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGln 217
Db 1407 -----ATCAATGGCTTAAATGTCACAGAAATCCGTGCACTTTCTTAAGAG 1451
Qy 218 GluGlnLysPheProLeu----- 223
Db 1452 GAACCTCAGATGCGCTTACACAAAGAGACCTTGAATTGGCCCTAAAGAAATTTGCTAAG 1511
Qy 224 ---ValGlyAlaThrAlaValGluAlaPheGlu 233
Db 1512 TCTGTCTCTGCTGAGACTTGAGAGATGATGAA 1544

RESULT 14
US-10-449-902-28331
; Sequence 28331, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A020511-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.11
; SEQ ID NO 28331
; LENGTH: 1061
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; APPLICANT: The Institute of Physical and Chemical Research.
; DATABASE ACCESSION NUMBER: AK103773

; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-28331
Alignment Scores:
Pred. No.: 2.26 Length: 1061
Score: 80.50 Matches: 53
Percent Similarity: 37.7% Conservative: 92
Best Local Similarity: 21.5% Mismatches: 40
Query Match: 6.5% Indels: 63
DB: 6 Gaps: 11

US-10-817-483-2 (1-239) x US-10-449-902-28331 (1-1061)

Qy 7 PheGlyProThrCysThrArgIleLysThrSerThrAlaIleAla---LeuAlaGlnGlnThr 25
Db 54 TTCCTCTCGTGGTGGCCGCTCCCGGCTTTCACCTCATGCGACGCTTGAACGTAACG 113
Qy 26 GLyLeuProValLeuSerLeuAspArgValGlnCysAspProGlnLeuSerThrGlySer 45
Db 114 GGGCGAGTGGCTTCGGC---AGCGGACGAGGTACTCCGCGCGGTGCTGCTTCC 170
Qy 46 GLyArgProThrValGluGluLeuLysGlyThrThrArgLeuTyrLeuAspArg-- 64
Db 171 GGTGCGCTCTCCTTCCTTCACAGCCGCCAAGCGCATGTGAATTTGCGCGCGCTTC 230
Qy 65 ---ProLeuValLysGlyIle-IleThrAlaLysGlnAlaHisGluArgLeuIleAlaG 83
Db 231 GTCGACATCATTCGGCATTCGGCCATCGGCCATCACTGAGCTTGATCGGTTGTTCTTGG 290
Qy 83 VValHisAsnHisGluAlaLysGlyGlyLeuIleLeuGluGlyGlySerLeu 103
Db 291 TCTCCAC-----GCCACGGCAACCTCTG----- 315
Qy 103 uArgCysMetAlaGlnSerArgTyrTrpAsnAlaAspPheArgTrpHisIleIleArgAs 123
Db 316 -----CAGTCATGCGCGCGCTCGATCCGCAC-CGTGCTTCCGGAT 355
Qy 123 nGluLeuAlaAspGluGluSerPheMetSerValAlaLysThrArgValLysGlnMetLe 143
Db 356 CCAGTGTTC-----GCTGTGCGTGAAGGCGGACGCTGCTCCAGAT 397
Qy 143 uArgProSerAlaGlyLeuSerIleIleGlnGluLeuValGlnLeuTrpArgGluProAr 163
Db 398 TCGC-----TCAGCGCTCCGATGCGACGGCATGGGTGACGCTGTCAACAGCGCAA 451
Qy 163 gLeuArgPro----- 168
Db 452 GCTTCCCTTCGTCGAGCAGATCGGTGTGACGCGCGCTTCGTCGAGCAGGTGAT 511
Qy 168 uGluGlyIleAsp-----GlyTyrArgTyrAlaLeuPheAlaThrGlnAsnG 185
Db 512 TGTCTTATGATGAGATCTTGAAGTTCGAGATTTCTTATTTTGTGTTTACTGATCA 571
Qy 185 nIle-----ThrProAspMetLeuGlnLeuAspAlaAspMetGluAs 200
Db 572 GCTGGCGTCGACAGTACGAGTACGACGTGATGCTGATGATGATGACCTTCCAGAA 631
Qy 200 nLysLeuIleHisGlyIleAlaGlnGluPheLeuIleHisAlaArgArgGlnGlnLys 220
Db 632 CAAGCTGATCGACAGCCTATCA-----AGGAAACCCCAAG 667
Qy 220 sPheProLeuValGlyAla 226
Db 668 ATTTGACATGCTGTGTGCA 686

RESULT 15
US-10-449-902-18278
; Sequence 18278, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USBS THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 18278
; LENGTH: 2119
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK068682
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-18278

Alignment Scores:

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|------------------------|-------|---------------|------|
| Pred. No.: | 5.94 | Length: | 2119 |
| Score: | 80.50 | Matches: | 71 |
| Percent Similarity: | 38.4% | Conservative: | 47 |
| Best Local Similarity: | 23.1% | Mismatches: | 101 |
| Query Match: | 6.5% | Indels: | 89 |
| DB: | 6 | Gaps: | 14 |

US-10-817-483-2 (1-239) x US-10-449-902-18278 (1-2119)

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OY      13 GlyLysThrSerThraAlaIleAlaLeuAlaGlnGlnThrGlyLeuProValLeuSerLeu 32
Db      379 GGACCAAGATCCGGGCGCTCAACGGCTTCAACGCGGAGAGACTGCCGCTTCCACCG 438
OY      33 AsparGValGlnCysCysProGlnLeuSerThrGlySerGlyArg----- 47
Db      439 CCT--CTACAGCTTCTGCGACACCTACCGCGGGGATCCGTGGGCGCGCGCTCAAGCT 495
OY      48 -----ProThrValGlnGlnLeu 53
Db      496 CAACACGGCCACGACATCGCATCACTGGGCGGCGGCTCCACACGACGACGAGATG 555
OY      54 LysGlyThrThrArgLeu-TyrLeuAspAspArgProLeuValLysGlyIleIleThrAl 73
Db      556 CGAGGCTCTCGGAGATTCTGCTACGTCACACGAC-----ATCGTCTCTCGCCATCTCGAGCT 609
OY      73 alyseGlnAlaHisGlnArgLeuIle-----AlaGlnValHisAsnHisGlnAlaL 90
Db      610 CCTCAAAATPCCACCAAGCGTGTCTCTATGTGATATCGATATCCACCATGGGAGATGTGT 669
OY      90 sGlyGlyLeuIleLeuGlnGly-----GlySerIleSerLeuLeuArgCysMet----- 106
Db      670 -GGAAGAGCGCTTTCACACGACGACGAGGTATGACGCTCTGTTCCACAAGTTTGGGG 728
OY      107 -----AlaGlnSerArgTyrTrp-AsnAlaAspPheArgTyrHisI 120
Db      729 ATTATTTCCCGGGGACCGGGGACATTCGCGATATTGGGCATCAAGGGGAAGTATTACT 788
OY      120 IeIleArgAsnGlnLeu-----AlaAspGlnGlnSerPheMetSerValAlaLys 137
Db      789 CTCTGAATGTCCTCGTTGACGACGCGTATGACGACGAGAGCTACAGTCGTTGTCACGC 848
OY      137 hr-----ArgValLysGlnMetLeuArgProSerAla----- 147
Db      849 CGATCATGGGGAAGGATGAGAGGTTTTCGCTGCGCGGCGGCTGCTCAAGTCGCGTG 908
OY      148 -----GlyLeuSerIle-----IleGln 154
Db      909 CGGACTCTCTCGGGGTAGATGAGTTGGGTTGCTTCAACTGCAATCAGGGGCCACGCGG 968
OY      154 IuLeuValGlnLeuThrPargLupProArgLeuArgProIleLeuGlnGlyIleAspGlyT 174
Db      969 AATGCGTAGATTCAATAGAGTCTTCAATATCCCGCTGTGCTGCTGGTGGTGGTGGT 1028
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OY      174 YArg-----TyrAlaLeuLeuPheAlaThrGlnAsnG 185
Db      1029 ATACCATAGAAGATTTGCGCGGTGTGGTGTCTATGACACAGAGATTGCATTTGGTCATG 1088
OY      185 IuIleThr-----ProAspMetLeu 192
Db      1089 AGCTCACTGACAAAGATGCTCCAAATGAGTATTTGAGTACTTTGGTCCAGATTTATACAC 1148
OY      192 euGlnLeu---AspAlaAspMetGluAsnLysLeuIleHisGlyIleAlaGlnGluPhe 211
Db      1149 TTCATGTTGCACCAAGTACATGAGAGACAAAACACACGCGCAGAGTTGATGAT----- 1204
OY      211 euIleHisAlaArgArgGlnGlnGlnLysPheProLeuValGlyAlaThrAlaValGlu 231
Db      1205 --ATAAGATCAAGACTTCTTGTATTAATTTCAAAACCTTCGACATGCTCCTACGCTCAAT 1262
OY      231 IaPheGlnGlyProPro 236
Db      1263 TTCAAAGCGACCCCT 1279
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Search completed: June 26, 2006, 20:40:50
Job time : 45 secs

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| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|-----------|------------------------|
| 1 | 1919 | 100.0 | 1919 | 2 | CQ995587 | CQ995587 Sequence |
| 2 | 1919 | 100.0 | 1919 | 15 | ABR1LT | X14410 Agrobacterium |
| 3 | 1104.8 | 57.6 | 206479 | 15 | AB016260 | AB016260 Agrobacterium |
| 4 | 1093.8 | 57.0 | 9931 | 15 | AB007927 | AB007927 Agrobacterium |
| 5 | 1093.8 | 57.0 | 10377 | 15 | AE005419 | AE005419 Agrobacterium |
| 6 | 1089.8 | 56.8 | 1997 | 15 | AB025109 | AB025109 Agrobacterium |
| 7 | 1060.8 | 55.3 | 29554 | 15 | ATU237588 | AJ237588 Agrobacterium |
| 8 | 976.6 | 50.9 | 1983 | 15 | ATU237588 | X00639 Agrobacterium |
| 9 | 958.4 | 49.9 | 24585 | 2 | BD016312 | BD016312 Method of |
| 10 | 958.4 | 49.9 | 24585 | 2 | E00404 | E00404 T1 plasmid |
| 11 | 958.4 | 49.9 | 24585 | 2 | E00546 | E00546 DNA fragment |
| 12 | 958.4 | 49.9 | 24585 | 2 | AR364803 | AR364803 Sequence |
| 13 | 958.4 | 49.9 | 24585 | 15 | ATACH5 | X00493 Agrobacterium |
| 14 | 958.4 | 49.9 | 194140 | 15 | AF242881 | AF242881 Agrobacterium |
| 15 | 956.8 | 49.9 | 1988 | 15 | ATTMR | X00010 Agrobacterium |
| 16 | 908.6 | 47.3 | 2724 | 15 | AB031422 | AB031422 Agrobacterium |
| 17 | 897 | 46.7 | 6482 | 15 | AY1AAN | X77327 A.vitis laevis |
| 18 | 877.8 | 45.7 | 14960 | 15 | AV083986 | U83986 Agrobacterium |

| | | | | | | | |
|---|----|-------|------|--------|----|-----------|-------------------|
| C | 45 | 189 | 9.8 | 10165 | 15 | AE009435 | Agrobacteri |
| C | 44 | 189 | 9.8 | 2171 | 15 | AE007942 | Agrobacteri |
| C | 43 | 189 | 9.8 | 1403 | 15 | ATTZS1 | Agrobacteri |
| C | 42 | 189 | 9.8 | 1403 | 15 | 105195 | Sequence 1 |
| C | 41 | 190.6 | 9.9 | 206479 | 15 | AB016260 | Agrobacte |
| C | 40 | 190.6 | 9.9 | 1413 | 15 | ATTZS | Agrobacte |
| C | 39 | 194.6 | 10.1 | 4660 | 15 | AB025110 | Agrobacte |
| C | 38 | 198.2 | 10.3 | 813 | 15 | ARTZSG | Agrobacte |
| C | 37 | 203.8 | 10.6 | 4679 | 15 | ATP10DNA | Agrobacte |
| C | 36 | 216 | 11.3 | 3271 | 15 | IS41PYVT | Agrobacte |
| C | 35 | 231.2 | 12.0 | 584 | 15 | 118499 | Sequence 2 |
| C | 34 | 252 | 13.1 | 1339 | 15 | ATU19150 | Agrobacte |
| C | 33 | 268.6 | 14.0 | 420 | 15 | T1P2MR | Plasmid pTi |
| C | 32 | 305.4 | 15.9 | 2544 | 2 | AR564457 | Sequence |
| C | 31 | 539.4 | 28.1 | 747 | 2 | AR564455 | Sequence |
| C | 30 | 545.4 | 28.4 | 723 | 2 | AR564460 | Sequence |
| C | 29 | 546.6 | 28.5 | 3183 | 2 | T175096 | Sequence 1 |
| C | 28 | 549.2 | 28.6 | 3182 | 2 | AR201516 | Sequence |
| C | 27 | 583.8 | 30.4 | 723 | 2 | C0899250 | Sequence |
| C | 26 | 693.4 | 36.1 | 1296 | 15 | T1P2R | Ti plasmid |
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| ACCESSION | Sequence 1 from Patent WO2004090143. |
| VERSION | CQ895587 |
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| ORGANISM | Agrobacterium tumefaciens (Rhizobium radiobacter) Agrobacterium tumefaciens Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium. |
| REFERENCE | 1 |
| AUTHORS | Habben,J.E., Zinselmeyer,C., Tomes,D.T., Abbitt,S.E., Helentjaris,T.G. and Niu,X. |
| TITLE | Modulation of cytokinin activity in plants |
| JOURNAL | Patent: WO 2004090143-A 1 21-OCT-2004; |
| PIONEER | HI-BRED INTERNATIONAL, INC. (US) |
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ORIGIN

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VERSION X14410.1 GI:38689
KEYWORDS ipt gene; isopentenyl transferase; transferase.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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REFERENCE 1 (bases 1 to 1919)
AUTHORS Strabala,T.U., Bednarek,S.Y., Bertoni,G. and Amasino,R.M.
TITLE Isolation and characterization of an ipt gene from the Ti plasmid
B0542
JOURNAL Mol. Gen. Genet. 216 (2-3), 388-394 (1989)
PUBMED 2747621
REFERENCE 2 (bases 1 to 1919)

AUTHORS Strabala, T.
TITLE Direct Submission
JOURNAL Submitted (02-FEB-1989) Strabala T., Department of Biochemistry,
University of Wisconsin Madison, 420 Henry Mall, Madison WI 53706
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| VERSION | AB016260.1 GI:6498173 | | |
| KEYWORDS | . | | |
| SOURCE | Agrobacterium tumefaciens (Rhizobium radiobacter) | | |
| ORGANISM | Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium. | | |
| REFERENCE | 1 Hattori,Y., Suzuki,K., Uraji,M., Ohta,N., Katoh,A. and Yoshida,K. Genome structure of pTi-SAKURA (I): strategy for DNA sequencing of a Japanese cherry-Ti plasmid | | |
| AUTHORS | Nucleic Acids Symp. Ser. 37, 159-160 (1997) | | |
| PUBMED | 9586048 | | |
| JOURNAL | Hattori,Y., Suzuki,K., Ohta,N., Uraji,M., Katoh,A. and Yoshida,K. Genome structure of pTi-SAKURA (V): Complete nucleotide sequence of plasmid pTi-SAKURA's vir region in Agrobacterium tumefaciens | | |
| REFERENCE | 2 Nucleic Acids Symp. Ser. 39, 265-266 (1998) | | |
| AUTHORS | 3 Ohta,N., Suzuki,K., Hattori,Y., Uraji,M., Katoh,A. and Yoshida,K. Genome structure of pTi-SAKURA (III): Characteristics of T-DNA | | |
| PUBMED | 9524202 | | |
| JOURNAL | Uraji,M., Suzuki,K., Ohta,N., Hattori,Y., Katoh,A. and Yoshida,K. Nucleic Acids Symp. Ser. 39, 185-186 (1998) | | |
| REFERENCE | 4 Uraji,M., Suzuki,K., Ohta,N., Hattori,Y., Katoh,A. and Yoshida,K. Genome structure of pTi-SAKURA (IV): Characteristics of tra region | | |
| AUTHORS | 5 Suzuki,K., Ohta,N., Hattori,Y., Uraji,M., Katoh,A. and Yoshida,K. Novel structural difference between nopaline- and octopine-type trb genes: construction of genetic and physical map and sequencing of trb/trai and rep gene clusters of a new Ti plasmid pTi-SAKURA | | |
| REFERENCE | 6 Suzuki,K., Ohta,N., Hattori,Y., Uraji,M., Katoh,A. and Yoshida,K. Biochim. Biophys. Acta 1396 (1), 1-7 (1998) | | |
| PUBMED | 9524202 | | |
| JOURNAL | Suzuki,K., Hattori,Y., Uraji,M., Ohta,N., Iwata,K., Murata,K., Kato,A. and Yoshida,K. Complete nucleotide sequence of a plant tumor-inducing Ti plasmid | | |
| REFERENCE | Gene 242 (1-2), 331-336 (2000) | | |
| AUTHORS | 7 (bases 1 to 206479) Suzuki,K. and Yoshida,K. Direct Submission | | |
| PUBMED | Submitted (22-JUL-1998) Kazuo Yoshida, Hiroshima University, Faculty of Science, Kagamiyama 1-3-1, Higashihiroshima-shi, Hiroshima 739, Japan (E-mail:khsuzuki@ipc.hiroshima-u.ac.jp, Tel:0824-24-7456, Fax:0824-24-0733) | | |
| JOURNAL | On or before May 14, 2001 this sequence version replaced gi:2982699, gi:2982703. Location/Qualifiers | | |
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ACCESSION AE007927 AE007871
VERSION AE007927.2 GI:16271969
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ORGANISM Agrobacterium tumefaciens str. C58
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE
AUTHORS Hinkle,G., Slater,S.C. and Goodner,B.
TITLE Complete Genome Sequence of Agrobacterium tumefaciens C58
(Rhizobium radiobacter C58), the Causative Agent of Crown Gall
Disease in Plants
COMMENT
FEATURES
source
1. .9931
Location/Qualifiers
On Oct 19, 2001 this sequence version replaced gi:15163470.

JOURNAL
REFERENCE 2 (bases 1 to 9931)
AUTHORS Hinkle,G., Slater,S.C. and Goodner,B.
TITLE Direct Submission
JOURNAL Submitted (14-AUG-2001) Cereon Genomics, 45 Sidney Street,
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On Oct 19, 2001 this sequence version replaced gi:15163470.
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ORIGIN

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RESULT 5

AE009419

LOCUS

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

10377 bp DNA linear BCT 28-MAY-2004
Agrobacterium tumefaciens str. C58 Ti plasmid, section 2 of 21 of
the complete sequence.
AE009419 AE008690
AE009419.1 GI:17744019
Agrobacterium tumefaciens str. C58
Agrobacterium tumefaciens str. C58
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
1 (bases 1 to 10377)
Wood, D.W., Secubal, J.C., Kaul, R., Monks, D., Chen, L., Wood, G.E.,
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TITLE
Zhao Z., Dolan M., Tingey S.V., Tomb J., Gordon M.P., Olson M.V.
and Nester E.W.
The genome of the natural genetic engineer Agrobacterium
tumefaciens C58
JOURNAL
Science 294 (5550), 2317-2323 (2001)
PUBMED
11743193
AUTHORS
2 (bases 1 to 10377)
Wood D.W., Setubal J.C., Kaul R., Monks D., Chen L., Wood G.E.,
Chen Y., Woo L., Kitajima J.P., Okura V.K., Almeida N.F. Jr.,
Zhou Y., Boyee D. Sr., Chapman P., Glendenning J., Deatherage G.,
Gillet M., Grant C., Guencher D., Kutayvin T., Levy R., Li M.,
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Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C.,
Zhao Z., Dolan M., Tingey S.V., Tomb J., Gordon M.P., Olson M.V.
and Nester E.W.
Direct Submission
Submitted (27-SEP-2001) Department of Microbiology, University of
Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
98195-7242, USA
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ORIGIN

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DEFINITION complete cds.
ACCESSION AB025109
VERSION AB025109.1 GI:4586309
KEYWORDS isopenentenyl transferase.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE 1 (bases 1 to 1997)
AUTHORS Kasahara,T., Sugita,K., Ebinuma,H., Endo,S., Kawakita,A. and
Moriwae,N.
TITLE Agrobacterium tumefaciens plasmid pO22 isopenentenyl transferase (ipt)
gene
JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 1997)
AUTHORS Kasahara,T., Sugita,K., Ebinuma,H., Endo,S., Kawakita,A. and
Moriwae,N.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-1999) Takehide Kasahara, Nippon Paper Industries

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Fax: 81-3-3914-3350)

FEATURES

Location/Qualifiers

1. 1997

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ORIGIN

Query Match 56.8%; Score 1089.8; DB 15; Length 1997;
Best Local Similarity 84.9%; Pred. No. 0;
Matches 1270; Conservative 0; Mismatches 212; Indels 13; Gaps 4;

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LOCUS Agrobacterium tumefaciens Ti plasmid pTiC58 T-DNA region.
DEFINITION Agrobacterium tumefaciens
ACCESSION AJ237588
VERSION AJ237588.1 GI:5042179
KEYWORDS acrocinopine synthase; agrocinopine synthase; IAH; isopenentenyl transferase; nopalline synthase; ornithine cyclodeaminase; protein 6a; protein 6b; torf1 gene; torf10 gene; torf11 gene; torf12 gene; torf13 gene; torf14 gene; torf15 gene; torf16 gene; torf17 gene; torf18 gene; torf19 gene; torf2 gene; torf20 gene; torf21 gene; torf22 gene; torf3 gene; torf4 gene; torf5 gene; torf6 gene; torf7 gene; torf8 gene; torf9 gene; tryptophan 2-monooxygenase.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium.

REFERENCE
1

AUTHORS Gielen J., Terryn N., Van Montagu M. and Villarroel R.
TITLE Complete nucleotide sequence of the T-DNA region of the plant tumor
inducing Agrobacterium tumefaciens Ti plasmid pTiC58
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 29524)
AUTHORS Gielen J.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-1999) Gielen J., Genetics, VIB/UG, KU
Leuven, Belgium
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LOCUS ATWPR1 1983 bp DNA linear BCT 18-APR-2005
DEFINITION Agrobacterium tumefaciens pTi37 T-DNA tmr locus.
ACCESSION X00639
VERSION X00639.1 GI:944822
KEYWORDS cytokinin; plasmid.
SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Agrobacterium.
REFERENCE 1 (bases 1 to 1982)
AUTHORS Goldberg, S.B., Flick, J.S. and Rogers, S.G.
TITLE Nucleotide sequence of the tmr locus of Agrobacterium tumefaciens
PTi T37 T-DNA
JOURNAL Nucleic Acids Res. 12 (11), 4665-4677 (1984)
COMMENT PUBLISHED On Aug 15, 1995 this sequence version replaced gi:39174.
FEATURES
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ORIGIN
polyA_signal 1418..1422

Query Match 50.9%; Score 976.6; DB 15; Length 1983;
Best Local Similarity 82.4%; Pred. No. 1.7e-305;
Matches 1233; Conservative 0; Mismatches 219; Indels 45; Gaps 8;

QY 1 GGATCCCGCTTAACAAGTATGACGCTTTTGTAAATGCAATTAATGCAATCTGATGTTT 60
DB 1 GGATCCTGTACAAAGTATGACGCTTTTGTAAATGCAATTAATGCAATCTGATGTTT 60
QY 61 AATAACGAATGTAATGGCGTA---GAAATATGATTTTATTTATTTATCTTTCATAT 116
DB 61 AACAACGAAGTAATGGCGTA---GAAATATGATTTTATTTATTTATCTTTCATAT 120
QY 117 GTTGAAGTTGCAATTAATGCTAATGTAATAATTAAATAATTAATGATGCGCATTTGT 176
DB 121 GTTGAAGGCTGCATTAATGATGATTAATTAATAATTAATTAATGATGCGCATTT 178
QY 177 TCAATGGCGCGCTATTTCAAAAATATCTTGTGATTTTGTACGAGAACAGCATGCGAG 236
DB 179 TGAATGGCACTGTTATTTCAACATATCTTGTGATTTGTTCATG---ACAGACCTGCA 236
QY 237 GAAGTAATTAAGAAGCGCTGTTGTAAGAATGCTATCATATGTCGCCAGCTATAGGCG 296
DB 237 GAAGTAATTAAGAAGCGCTGTTGTAAGAATGCTATCATATGTCGCCAGCTATAGGCG 295
QY 297 CATTTAAGTCAATGTAATGAGCGCGCTTATTTTGACGCTCATCAAAACCAATAT 356
DB 296 -----AATTTGAGCGTCAGACCTTAATCAATAT 324
QY 357 AAAAAATATCTCACTGTGCGCAGCAATGATGATATAACCGAGA-AAAGTAGAGATA 415
DB 355 ACAAATATCTCACTGTGCGCAGCAATGATGATATCAAGCGCAGCAAAATGCGGTAAAG 384

QY 416 ATGCGGAAAAAAGTCGCGAGATGAGCATGAATAGCGGCTCCGTAATTGCTGATTAAGTA 475
DB 385 ATGCGGAAAAAAGTCGCGAGATGAGCATGAATAGCGGCTCCGTAATTGCTGATTAAGTA 443
QY 476 GCTTATTTGACTTAAGGCTGCTCGTTAGTGAACAAATGCTTTCAAGAGACAGCCAT 535
DB 444 GCTTATTTGACTTAAGGCTGCTCGTTAGTGAACAAATGCTTTCAAGAGACAGCCAT 503
QY 536 GCCCAACACTTTGTAAGAAACAAAGTGCCTTTTGGAGAAACCTTAAGCCACTTGCTCT 595
DB 504 GCCCAACACTTTGTAAGAAACAAATGTC-TTTGGAGAGAGCGGTAAACAGTTCCTCT 562
QY 596 TCAAGAGGAATATGAGGAAGAAATATTAAGCTCTGTAAGCACTTCTCTTGCA 655
DB 563 TCAATTAAGGAATCTGAGAGGCAATATTAAGCCCTGTAAGTACATTTCTTAATCCA 622
QY 656 AAAATCAATTTGATTTCAACATATGCG--AAGACGATGATCTACGCTAAATTTTCGAT 713
DB 623 AAAATCAATTTGATTTCAAGATACCGCAAAAACCTTAATGATCTGCTTAATTTTCGAT 682
QY 714 CCAACTTGACAGAGAAAGACATGCACTGAGATAGCTTTGCCAGACACTGCGCTCCA 773
DB 683 CCAACTTGACAGAGAAAGACGTCGACCGCGGTAGCTCTTGCCAGACACTGCGCTCCA 742
QY 774 GTTCTCTGCTGATCGGCTCCATGCTGTCTCTCAATATCAACCGGAAGCGGCGCA 833
DB 743 GTTCTCTGCTGATCGGCTCCATGCTGTCTCTCAAGCTGTCAACCGGAAGCGGCGCA 802
QY 834 ACAGTGAAGAACTGAAGAAAGACACTGCTGTGACCTTGATGATGCGCTTTGTAAG 893
DB 803 ACAGTGAAGAACTGAAGAAAGACAGCCCTCTATACCTTGAATGATGCGCTCTGGAAG 862
QY 894 GGTATCATTTACAGCCAGCAAGCTCATGAACGCTCATTTGCGAGGTGACATACAGAG 953
DB 863 GGTATCATTTACAGCCAGCAAGCTCATGAAGCTCATGAGGAGAGGTGATATATATGAG 922
QY 954 GCCAAAGCGGCGCTTATTTTGAAGAGATCTATCTGCTGCTCAGGTGATGCGGCA 1013
DB 923 GCCCAAGCGGCGCTTATTTTGAAGAGATCTATCTGCTCCTCAAGTGCATGCGGCA 982
QY 1014 AGTCGTTATTTGAGAGCGGATTTTGTGGCATATTTATGCAACGAGTTAGACAGAG 1073
DB 983 ACAGATTAATGAGAGCGGATTTTGTGGCATATTTATGCAACGAGTTAGACAGAG 1042
QY 1074 GAGACTTCATAGCGGTGCGCAAGACAGAGTTAAGCAGATGTTACGCCCTCTGCAAGT 1133
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DB 1163 AAGAGATCGAGATATCGATATGATGCAATGTGTTGCTAGCCAGAACCAAGATCAATCC 1222
QY 1254 GATATGCTAATTTGACCTGACGACAGATATGAGAAATTAATGATTTACAGCTATCGCTCAG 1313
DB 1223 GATATGCTAATTTGACCTGACGACAGATATGAGAAATTAATGATTTACAGCTATCGCTCAG 1282
QY 1314 GAGTTTCTAATTCATGCGGCTGACAGAAACAGAAATTCCTTTGAGGCGCGACAGCT 1373
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QY 1374 GTGGAAGGTTGGAAGACCAACATTTGGAATGATATGATTTGCAACAGTTTGTGTCAG 1433
DB 1343 TAGGACGAGTTGGAAGATCATCTCGAATGATTTAGTTTTCACCACTCCGCTCAC 1402
QY 1434 ACTGTGCTATTTGGAATGAGATGTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1490
DB 1403 ACTGTGCTATTTGGAATGAGATGTTTTCGAATTTGTTTGTGTTGTTGTTGTTGTTGTTG 1459

| | | | | | |
|------------|---|---|------|--------|-----------------|
| RESULT 9 | BD016312 | 24595 bp | DNA | linear | PAT 27-AUG-2002 |
| LOCUS | BD016312 | | | | |
| DEFINITION | Method of promoting plant transcription by using octopine T-DNA promoter. | | | | |
| ACCESSION | BD016312.1 | GI:22557450 | | | |
| VERSION | BD016312 | | | | |
| KEYWORDS | Agrobacterium tumefaciens (Rhizobium radiobacter) | | | | |
| SOURCE | Agrobacterium tumefaciens | | | | |
| ORGANISM | Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Agrobacterium. | | | | |
| REFERENCE | 1 (bases 1 to 24595) Barker, R.F. and Kemp, J.D. Method of promoting plant transcription by using octopine T-DNA Patent: JP 2001190289-A 1 17-JUL-2001; | | | | |
| AUTHORS | RICHARD F BARKER, JOHN D KEMP | | | | |
| TITLE | PC C12N15/09, A01H5/00, C12N5/10, C12N15/00, C12N5/00 CC Method of promoting plant transcription by using octopine T-CC | | | | |
| JOURNAL | Mycogen Plant Science Inc | | | | |
| COMMENT | OS Agrobacterium tumefaciens PN JP 2001190289-A/1 PD 17-JUL-2001 PF 22-NOV-2000 JP 2000356816 PR 18-NOV-1983 US 553786 PI RICHARD F BARKER, JOHN D KEMP PC C12N15/09, A01H5/00, C12N5/10, C12N15/00, C12N5/00 CC Method of promoting plant transcription by using octopine T-CC | | | | |
| FEATURES | FT source Location/Qualifiers 1..24595 /organism="Agrobacterium tumefaciens". /mol_type="genomic DNA" /db_xref="taxon:358" | | | | |
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| Oy | 1 | GGATCCGCTTACAGTATTTGACGCTTTGTAATTTGCATATTTAAATGCAATCTGATGTTT | 60 | | |
| Db | 8082 | GGATCCGCTTACAGTATTTGACGCTTTGTAATTTGCATATTTAAATGCAATCTGATGTTT | 8141 | | |
| Oy | 61 | AATAACGAATGTATGCGGTAAATATGATTTTATTGATTTATTCCTTCACTATGTTG | 120 | | |
| Db | 8142 | AACAACGAACGTAAATGCGGTAAATATGATTTTATTGATTTATTCCTTCACTATGTTG | 8200 | | |
| Oy | 121 | AAGTTTGAATTAATGCTAATGTAATTTAAATTAATGTAATGTAATGTAATGTAATGTAAT | 180 | | |
| Db | 8201 | GAGTGGCGCATTAATGTAATGTAATTTAAATTAATGTAATGTAATGTAATGTAATGTAAT | 8259 | | |
| Oy | 181 | ATGCGCGCGCTTATTTCAA-----AAATATCTTTGATTTTGTACAGAGCAACGACTGCA | 235 | | |
| Db | 8260 | ATGCGACGCTTATTTCAAACCAATGTAATTTGTAATTTTAAATTAATTAATTAATTAATTA | 8319 | | |
| Oy | 236 | GGAAGTAATTAAGACGCTGTTGTTAAGAAATTCATATGATGCTCCAGCTATAGGG | 295 | | |
| Db | 8320 | GGAAGTAATTAATGACGCGTGTGTTAAGAAATTCATATGATGCTCCAGCTATAGGG | 8379 | | |
| Oy | 296 | CCATTTAAGTTCAATGTGAATAGCGCCCTTATTTGAGCTGCATCAATCAATCAATAT | 355 | | |
| Db | 8380 | ACAATTAAGTCAA--TTGTAATAGTCTCCCTTATTTTAACGACTCACTTAATCAAGTAT | 8436 | | |
| Oy | 356 | TAAAAAATATCTCACTCTGCGCCAGCAATGTAATTAACGCGAAGAAAGTAGATTA | 415 | | |
| Db | 8437 | TACAAAATATCTCACT-TTTGTCTGTAATGATGTAATTAACGAACTGAATAGTCAAGTA | 8495 | | |
| Oy | 416 | ATGCGCGAAGAAACGTCGCGAGTGCGATGAATAGCGGCTCCGTAATGCTGATTTAGTCA | 475 | | |
| Db | 8496 | AACGTGAAAAACGCTATAGAGTGCGATGATTAATTTCTCTGCACTGCCAATTTATTTCA | 8555 | | |
| Oy | 476 | GCTTATTGTGACTTAAGGGTCCCTCGTTAGTGAACAATTTGCTTTCAAGGAGACGCAAT | 535 | | |

| | | | | | |
|------------|--------------------------|--|------|--------|-----------------|
| Db | 8556 | GCTTATTGTGACTTAAGGTGCTCTTGGTATGTAACAATTTGCTTTCAAGGAGACGCAAT | 8615 | | |
| Oy | 536 | GCCCCACACTTTGTTGAAAAACAAGTTCCTTTTGGGAAAGAACTTAAGCCACTTGTCT | 595 | | |
| Db | 8616 | GCCCCACACTTTGTTGAAAAACAAGTTCCTTTTGGG-ATACGGTAAAGCCAGTTGCACT | 8674 | | |
| Oy | 596 | TCAAGAGGAATATCGAGGAAGAAATTTAATACAGCTCTGGT-ACAGACTTCTTGTGCG | 654 | | |
| Db | 8675 | TCAATTAATGAAATTTTCAAGG-AGACAAATTAACCGCTCTGATTAACACAAATTTCTTAATAT | 8733 | | |
| Oy | 655 | AAAAATCAATTTGATTTCAACATATCCG--AAGACCATGGATCTAGCTTAATTTTGG | 712 | | |
| Db | 8734 | AAAAATCAATTTGATTTCAATATCTGCAAAAAAATTATGACCTGCAATTAATTTTGG | 8793 | | |
| Oy | 713 | TCCAACTTGCACAGAAAAACATGACTGCAATGCTTTGCGCAGACAGACTGCGCTCC | 772 | | |
| Db | 8794 | TCCAACTTGCACAGAAAAACATGACTGCAATGCTTTGCGCAGACAGAGGCTTCC | 8853 | | |
| Oy | 773 | AGTCTCTCGTGCATGCGCTCCCAATGCTGCTTCAATCAATCAACCGGAAGCGGCGAC | 832 | | |
| Db | 8854 | AGTCTCTCGTGCATGCGGCTCCCAATGCTGCTTCAATCAATCAACCGGAAGCGGCG | 8913 | | |
| Oy | 833 | AACAGTGAAGAACTGAAGAGAAAGCACTGCTGATGCTGATGATGCTGCTTGGTAA | 892 | | |
| Db | 8914 | AACAGTGAAGAACTGAAGAGAAAGCAAGCTGCTGATGCTGATGATGCTGCTTGGTAA | 8973 | | |
| Oy | 893 | GGGTATCATTAACAGCAAGCAAGCTCATGAAGGCTCATTTGGAGGTGCAATACAG | 952 | | |
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| Oy | 953 | GCCCAAGGCGGCTTATTTCTTGAGGAGAAATCATCTCTGCTCAGTGTGCAATGCGCA | 1012 | | |
| Db | 9034 | GGCCAAAGCGGCTTATTTCTTGAGGAGAAATCAACCTGTTGCTCAATGCAATGCGCG | 9093 | | |
| Oy | 1013 | AAGTGTATTGGAACGCGGATTTTCTGTCATATTATTGCAACAGAGTTAGACAGCA | 1072 | | |
| Db | 9094 | AACAGCTATTGAGTGCAGATTTTCTGTGCAATTTATTCGCCAAGATTAACCGACCA | 9153 | | |
| Oy | 9154 | AGAAGCTTCAATGAAGAGGCGCAAGGCGAGAGTTAAGCAAGATGTTGCAACCCGCTG | 9213 | | |
| Db | 1133 | TCTTTCTATTATCCAAAGTGTGTTCACTTTTGAAGGAAGCTCGCTGAGGCCATATCT | 1192 | | |
| Oy | 9214 | CCATTCTAATTAATTAAGAGTGTGTTATCTTTGAAATGAACCTGCGCTGAGGCCATCT | 9273 | | |
| Db | 1193 | GGAAGGATCGATGATATCGATATGCTGCTATTTGCTACCCAGAACCATCAACGCC | 1252 | | |
| Oy | 9274 | GAAAGATTCGATGATATGCAATATGCAATATGCAATGTTGTTGCTAGCCAGAACGATCA | 9333 | | |
| Db | 1253 | CGATATGCTATTGAGCTCGACGCAAGATATGAGAAATTAATGATTCACGGTATGCTCA | 1312 | | |
| Oy | 9334 | AGATATGCTATTGAGCTTGAACGCAAAATATGAAAGTGAATGATTAATGGAATGCTCA | 9393 | | |
| Db | 1313 | GGAATTTCTAATCCATGCGCGTCCAGAGAAACAATAATTCCTTTTGGTGGCGCGACGC | 1372 | | |
| Oy | 9394 | GGAATTTCTAATCCATGCGCGTCCAGAGAAACAATAATTCCTTTTGGTGGCGCGCGC | 9453 | | |
| Db | 1373 | TGTGGAAGCGTTTGAAGGACCAACATTTGCAATGATAGATGATGCAACAGATTTTGTTC | 1432 | | |
| Oy | 9454 | TTTGACAGGATTCGAAGGTCAATCCGTTGGAATGATTAATGATTAATGATTAATGATTA | 9513 | | |
| Db | 1433 | GACTTGTGCTATTGAAATTAAGATGTTGCTTTTGTGTGTGTGTGTGTGTGTGTGTGT | 1490 | | |
| Oy | 9514 | CACCTGTCTTATCGATGATTAAGATGTTGATTAATGTTTGTGTGTGTGTGTGTGTGTGT | 9571 | | |
| RESULT 10 | | | | | |
| LOCUS | E00404 | 24595 bp | DNA | linear | PAT 29-SEP-1997 |
| DEFINITION | Ti plasmid T-DNA region. | | | | |
| ACCESSION | E00404 | | | | |

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VERSION      E00404.1 GI:2168687
KEYWORDS     JP 198515633-A/1..
SOURCE       Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM     Agrobacterium tumefaciens
              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
              Rhizobiaceae; Agrobacterium.
REFERENCE    1 (bases 1 to 24595)
AUTHORS      Garli, E.D., Deniau, P.S. and Richiyado, E.B.
TITLE        SELECTION USING OPINE SYNTHASE GENE
JOURNAL      Patent: JP 198515633-A 1 16-AUG-1985;
              AGURIJENETIKUSU RES ASSOC LTD
COMMENT      OS Agrobacterium tumefaciens
              PN JP 1985156333-A/1
              PD 16-AUG-1985
              PF 14-SEP-1984 JP 1984193841
              PR 14-SEP-1983 US 83 532280
              PI GARII EB DAARU, DENISU DABURIYU SATSUTON,
              RI RICHIIYADO EFU BEIKAA
              PC A01H1/00,C12N5/00,C12N15/00,(C12N5/00,C12R1:91); CC
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              CC Topology: Linear;
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ORIGIN
Query Match 49.9%; Score 958.4; DB 2; Length 24595;
Best Local Similarity 81.5%; Pred. No. 1,4e-299;
Matches 1221; Conservative 0; Mismatches 261; Indels 16; Gaps 9;
QY 1 GGATCCCGTTACAGTATTTGACAGTTTGTAAATTCATATTAATGCAATCGATGTTT 60
DB 8082 GGATCTCTTTACAGTATTTGACAGTTTGTAAATTCATATTAATGCAATCTGATTTT 8141
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DB 8142 AACACGAACTGAATGCGGTA-AAAAATGTAATGTAATTTATTTATTTATTTATTTG 8200
QY 121 AAGTTGCAATTAATGCTAATGTAATTAATAATTAATGTAATGCTGCGCATTTGTCAA 180
DB 8201 GAGTGCGCATTAATGATGATTAATTAATAAAAA-TATTTACTGTCACATGACTAG 8259
QY 181 ATGGGCGCGTATTTCAA-----AAATATCTTTGATTTTGTACGAGACAACGACTGCA 235
DB 8260 ATGGACCTGTTATTTCAACATGAAATTTTGTGATTTTTTTACAAATAACATTAATTCGA 8319
QY 236 GGAAGTAAATAAAGACGCTGTTGTAAGAATTCCTATTCATATGTCGCCAGCTATAGGG 295
DB 8320 GGAAGTAAATATAGACCGCTGTTGTAATAAATTCGATCATATGCTTAATGAGG 8379
QY 296 CCATTTAAGTTCAATTTGTAATAGCGCCCTTAATTTGAGCTTCATCAATCAAAATAT 355
DB ||||||| | ||||||| ||||||| || ||||| ||||||| |||
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QY 356 TAAAAATATCTCACTCTGTGCGCCAGCAATGTAATTAATACCGCAAAAAAGTGAAGTAA 415
DB 8437 TACAAAAATATCTCACT-TTTGCTCAGTATGATGTAATACAGAACTGAATAGTAA 8495
QY 416 ATCGGGGAAAAACGTCGCGGATGTCAGTAATAGGGGCTCGCTATTCGTGATTAAGTCA 475
DB 8496 AACGTGAAAAACGTCATAGAGTGGCAATGATTAATTTCTTCGATTCGCAATTTATTTCA 8555
QY 476 GCTTATTTTGACTTAAGGGTGCCCTCGTTAGTGAACAAATGCTTTCAAGAGACAGCCAT 535
DB 8556 GCTTATTTTGACTTAAGGGTGCTTCCTCGTTAGTGAACAAATTTGCTTTCAAGAGACAGCCAT 8615
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DB 8675 TCATTAATGAATTTTCMAAG-AGACAAATATTAACCGCTCTGATTAACAAATTTCTTAATAT 8733
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DB 8794 TCCAACTTGCAAGAGAAAGACAGACCGCGATAGCTCTTGGCCAGACAGAGGCTTCC 8853
QY 773 AGTCTCTGCTCGATTCGCGCTTCCAATGCTGCTCTTAATATTAACCGGAAAGGGCGACC 832
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QY 833 AACAGTGAAGAACTGAAGAGAAAGAGACTGCTGTAACCTGTAATGCGCCCTTGTGTA 892
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LOCUS Sequence 1 from patent US 5428147.
ACCESSION AR364803
VERSION AR364803.1 GI:34427834
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 24595)
AUTHORS Barker, R.F. and Kemp, J.D.
TITLE Octopine T-DNA promoters
JOURNAL Patent: US 5428147-A 1 27-JUN-1995;
Mycogen Plant Science, Inc., San Diego, CA
FEATURES
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ORIGIN
Query Match 49.9%; Score 958.4; DB 2; Length 24595;
Best Local Similarity 81.5%; Pred. No. 1,4e-299;
Matches 1221; Conservative 0; Mismatches 261; Indels 16; Gaps 9;

Qy 1 GGATCCCGTTACAGATTTGCAAGTTTGTAAATTCATATTAATCAATCTGGATGTT 60
Db 8082 GGATCCTGTTACAGATTTGCAAGTTTGTAAATTCATATTAATCAATCTGATTTT 8141
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SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
ORGANISM Agrobacterium tumefaciens
REFERENCE Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
AUTHORS Rhizobiaceae; Agrobacterium.
TITLE 1 (bases 1 to 24595)
JOURNAL Barker, R.F., Idler, K.B., Thompson, D.V. and Kemp, J.D.
REFERENCE Nucleotide sequence of the T-DNA region from the Agrobacterium
AUTHORS tumefaciens octopine Ti plasmid pTi15955
TITLE 2 (bases 602 to 14237)
JOURNAL Plant Mol. Biol. 2, 335-350 (1983)
AUTHORS Glielen, J., De Beuckeleer, M., Seurinck, J., Deboeck, F., De Greve, H.,
Lemmers, M., Van Montagu, M. and Scheil, J.
TITLE The complete nucleotide sequence of the T-DNA of the Agrobacterium
JOURNAL tumefaciens plasmid pTiAch5
PUBMED EMBO J. 3 (4), 835-846 (1984)
REFERENCE 3 (bases 1 to 24595)
AUTHORS Turk, S.C., Nester, E.W. and Hooykaas, P.J.
TITLE The vira promoter is a host-range determinant in Agrobacterium
JOURNAL tumefaciens
PUBMED Mol. Microbiol. 7 (5), 719-724 (1993)
REFERENCE 4 (bases 1 to 24595)
AUTHORS Guevara-Garcia, A., Mosqueda-Cano, G., Arguello-Asciorga, G.,
Simpson, J. and Herrera-Estrella, L.
TITLE Tissue-specific and wound-inducible pattern of expression of the
mannopine synthase promoter is determined by the interaction
between positive and negative cis-regulatory elements
JOURNAL Plant J. 4 (3), 495-505 (1993)
PUBMED 8220492
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REFERENCE
AUTHORS 21 (bases 133963 to 138972; 176911 to 186244)
TITLE Skyler,J.L., Mantis,N.J., Kalojeraki,V.S. and Winans,S.C.
JOURNAL Direct Submission
Submitted (23-DEC-1997) Microbiology, Cornell University, Ithaca,
NY 14853, USA
REFERENCE
AUTHORS 22 (bases 22855 to 39243)
TITLE Winans,S.C.
JOURNAL Direct Submission
Submitted (03-AUG-1998) Microbiology, Cornell University, Wang
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REFERENCE
AUTHORS 23 (bases 62801 to 66985)
TITLE Oger,P.M.
JOURNAL Direct Submission
Submitted (29-DEC-1998) Crop Sciences, University of Illinois at
Urbana-Champaign, 361 ERMU, 1201, W. Gregory Dr., Urbana, IL 61801,
USA
REFERENCE
AUTHORS 24 (bases 110822 to 133968)
TITLE Zhu,J. and Winans,S.C.
JOURNAL Direct Submission
Submitted (18-AUG-1999) Section of Microbiology, Cornell
University, Wang Hall, Ithaca, NY 14853, USA
REFERENCE
AUTHORS 25 (bases 1 to 194140)
TITLE Zhu,J., Oger,P.M., Schrammeijer,B., Hooykaas,P.J., Farrand,S.K. and
Winans,S.C.
JOURNAL Direct Submission
Submitted (07-MAR-2000) Microbiology, Cornell University, Wang
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| | | | |
|----|------|--|------|
| Db | 8307 | CCATTCTATTATTCAGAGTGGTTTATCTTTGGAAATGAACCTGGCTGAGGCCCATTTCT | 8366 |
| Qy | 1193 | GGAAGGATCGATGATATCGATATGCCCTGCTATTTGCTAACCGAAGACGATACAGCC | 1252 |
| Db | 8367 | GAAAGAGATGATGATATCGATATGCCCTGCTATTTGCTAACCGAAGACGATACAGCC | 8426 |
| Qy | 1253 | CGATATGCTATTCAGCTCGACGAGATATGAGATTAATTGATTCACGGTATCGCTCA | 1312 |
| Db | 8427 | AGATATGCTATTCAGCTCGACCTTGACGAGAAATATGGAAGTATGATTAATGGAATCGCTCA | 8486 |
| Qy | 1313 | GGAGTTTCTATATCCATGCGCGCTCGACAGGAACAGAAATTCCTTGGTGGCGGACAGC | 1372 |
| Db | 8487 | GGAGTATTTCTATCATTCATCGCGGCCCAACAGGAACAGAAATTCCTTGGTGGCGGCGC | 8546 |
| Qy | 1373 | TGTGGAAGCGTTTGAAGACCACTTCGATGTGATGATTCACCAAGTTTGTTC | 1432 |
| Db | 8547 | TTTGAAGGATTCGAAGGTCATCGCTTGGGAATGATTAAGTTAGCGCAGCCGCGCTGG | 8606 |
| Qy | 1433 | GACTTTCGCTATTTGAATAGATGTT | |

| | | | |
|--|------|--|------|
| Best Local Similarity 81.4%; Pred. No. 48e-299; | | | |
| Matches 1220; Conservative 0; Mismatches 262; Indels 16; Gaps 9; | | | |
| Qy | 1 | GGATCCCGGTACAGATATTCACAGCTTTTGTAAATGCAATTAATGCAATTCGATGATGTT | 60 |
| Db | 1 | GGATCCGTTTACAGATATTCAGATGTTTATTAATTCATATTAATGCAATTCGATGATGTT | 60 |
| Qy | 61 | AATTAAGCAATGTAATGCGGTGAGAAATATGATTTATTAATTAATTAATTCACATATGTT | 120 |
| Db | 61 | AAACAAGCAAGTAAATGCGGTGAGAAATATGATTTATTAATTAATTAATTAATTAATG | 119 |
| Qy | 121 | AAGTTGCAATTAATATCTATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA | 180 |
| Db | 120 | GAGTGGCCCATATATATATATATATTAATTAATTAATTAATTAATTAATTAATTAATTA | 178 |
| Qy | 181 | ATGGCGCGGTATTTTCAA----AAATATCTTGATTTTGTACAGAGACACAGCTGCA | 235 |
| Db | 179 | ATGGCAGTGTATTTTCAAACCATGAAATTTGTGATTTTGTACATTAATTAATTAATTA | 238 |
| Qy | 236 | GGAATTAATTAAGACGCTGTTGTAAGAAATTCATATATGATTCGACGATATAGG | 295 |
| Db | 239 | GGAATTAATTAAGACGCTGTTGTAAGAAATTCATATATGATTCGACGATATAGG | 298 |
| Qy | 296 | CCATTTAAGTTCAATTTGAAATATGCGCCCTTATTTGACGTCTCAATCAATCAATAT | 355 |
| Db | 299 | ACAATTAAGTCAA---TTGTAATATGCTCTCCCTTATTTTAAGACTCACTATATCAAT | 355 |
| Qy | 356 | TAAATAATATCTACTGTCGCGCAGCAATGATTAATTAACGAGAAAGTAGAGTAA | 415 |
| Db | 356 | TACAAATATCTACT--TTTCGTAGATATGATTAATTAACGACTGAATAGTAAATGAA | 414 |
| Qy | 416 | ATGCGGAAAAACGTGCGCAGTGCATGAATAGCGGCTCCGATATGCTGATTAATCA | 475 |
| Db | 415 | AACGTGAAAAACGTCAATGAGTGCATGAATATATTCCTCTGATTTGCCAATTAATCA | 474 |
| Qy | 476 | GCTTATTTTGACTTAAGGATGCGCTCGTTAGTCAATATGCTTTCAAGAGACAGCAT | 535 |
| Db | 475 | GCTTATTTTGACTTAAGGATGCGCTCGTTAGTCAATATGCTTTCAAGAGACAGCAT | 534 |
| Qy | 536 | GCCCCACACTTTGTTGAAAAACAAGTTCCTTTTGGAGAAACCTAAAGCCACTGCTCT | 595 |
| Db | 535 | GCCCCACACTTTGTTGAAAAACAAGTTCCTTTTGGAGAAAGCCAGTTGACAT | 593 |
| Qy | 596 | TCAAGAGAAATATCGAGAAAGAAATTAACGCCCTGCT--ACACACTCTCTGTCGC | 654 |
| Db | 594 | TCAATTAATGATTTCAAAG--AGACAATTAACGCCCTGATTAACAATTTCTTAATAT | 652 |
| Qy | 655 | AAAATCAATTTGATTTCAACATATCGC--AAGACGATGATTAATGCTTAATTTTCG | 712 |
| Db | 653 | AAAATCAATTTGATTTCAATATATCTGCAAAAACTATGACCTGATCTAATTTTCG | 712 |
| Qy | 713 | TCCAATTCGACAGAAAGACATGACTGCGATAGCTTTGCCAGACAGATGCGCTCC | 772 |
| Db | 713 | TCCAATTCGACAGAAAGACAGACCGGATAGCTTTGCCAGACAGACAGGCGCTCC | 772 |
| Qy | 773 | AGTCTCTGCTGATGCGCTGCAATGCTGCTCACTATCAACCGGAGCGGCGAC | 832 |
| Db | 773 | AGTCTCTGCTGATGCGCTGCAATGCTGCTCACTATCAACCGGAGCGGCGAC | 832 |
| Qy | 833 | AACAGTGAAGAACTGAAGGAAGACATCGCTGTATCTTGATATGAGCTTTGTAA | 892 |
| Db | 833 | AACGTGAAGAACTGAAGGAAGACATCGCTGTATCTTGATATGAGCTTTGTAA | 892 |
| Qy | 893 | GCGTATCATTAACAGCAAGCAAGCTCATAGCGCTCATTTGCGAGGTGCAATYCA | 952 |
| Db | 893 | GCGTATCATTCAGCAAGCAAGCTCATATAGCTGATCGAGAGGTATATATATGA | 952 |
| Qy | 953 | GCGCAAGGCGGCTTATTTTGTAGGAGATCTATCTGTTGCTCAGTTCATGCGCA | 1012 |
| Db | 953 | GCGCAAGGCGGCTTATTTTGTAGGAGATCTATCTGTTGCTCAGTTCATGCGCGC | 1012 |
| Qy | 1013 | AAGTGTATTTGAACCGGATTTTGTGTCATATTAATTCGAAACAGATTAAGACAG | 1072 |
| Db | 1013 | AAGTGTATTTGAACCGGATTTTGTGTCATATTAATTCGAAACAGATTAAGACAG | 1072 |

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2006, 18:07:56 ; Search time 1130 Seconds
(without alignments)
11840.482 Million cell updates/sec

Title: US-10-817-483-1

Perfect score: 1919
Sequence: 1 ggcattccggtacaagctatg.....tacgcatcatatagacaagctt 1919

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_8:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
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- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*
- 15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1919 | 100.0 | 1919 | 13 | ADT92127 |
| 2 | 1089.8 | 56.8 | 1997 | 12 | AD055756 |
| 3 | 958.4 | 49.9 | 24596 | 1 | AAN50182 |
| 4 | 956.8 | 49.9 | 1988 | 6 | ABK12492 |
| 5 | 953.6 | 49.7 | 24593 | 1 | AAN50226 |
| 6 | 722 | 37.6 | 3017 | 3 | AAC86511 |
| 7 | 720.4 | 37.5 | 2722 | 3 | AAC86508 |
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| 10 | 720 | 37.5 | 721 | 3 | AAC86514 |
| 11 | 720 | 37.5 | 723 | 10 | ACF58155 |
| 12 | 717 | 37.4 | 717 | 13 | AD563261 |
| 13 | 583.8 | 30.4 | 723 | 13 | ADT62691 |
| 14 | 583.6 | 30.4 | 720 | 13 | AD562464 |
| 15 | 583.6 | 30.4 | 720 | 13 | AD559368 |
| 16 | 583.6 | 30.4 | 720 | 13 | AD562875 |
| 17 | 582.2 | 30.3 | 723 | 13 | ADR42934 |
| 18 | 582.2 | 30.3 | 723 | 13 | ADR42936 |

| | | | | | | | |
|----|-------|------|------|----|----------|----------|-----------|
| 19 | 582.2 | 30.3 | 723 | 15 | AEF15453 | AEF15453 | Isopenten |
| 20 | 582.2 | 30.3 | 723 | 15 | AEF15472 | AEF15472 | Isopenten |
| 21 | 582 | 30.3 | 720 | 13 | AD563295 | AD563295 | Bacterial |
| 22 | 582 | 30.3 | 720 | 13 | AD563280 | AD563280 | Bacterial |
| 23 | 580.6 | 30.3 | 723 | 13 | ADR42938 | ADR42938 | IPR-like |
| 24 | 580.6 | 30.3 | 723 | 15 | AEF15470 | AEF15470 | Isopenten |
| 25 | 578.8 | 30.2 | 720 | 13 | AD563275 | AD563275 | Bacterial |
| 26 | 578.8 | 30.2 | 720 | 13 | AD563279 | AD563279 | Bacterial |
| 27 | 578.8 | 30.2 | 720 | 13 | AD563294 | AD563294 | Bacterial |
| 28 | 577.4 | 30.1 | 723 | 15 | ADR42940 | ADR42940 | IPR-like |
| 29 | 577.4 | 30.1 | 723 | 15 | AEF15468 | AEF15468 | Isopenten |
| 30 | 577.2 | 30.1 | 2595 | 11 | ADJ98855 | ADJ98855 | IPR gene |
| 31 | 577.2 | 30.1 | 2595 | 11 | ADL73033 | ADL73033 | Agrobacte |
| 32 | 577.2 | 30.1 | 2595 | 14 | ADX69862 | ADX69862 | Isopenten |
| 33 | 577.2 | 30.1 | 9323 | 10 | ADJ99857 | ADJ99857 | Binary ve |
| 34 | 577.2 | 30.1 | 9323 | 14 | ADX69863 | ADX69863 | Plasmid p |
| 35 | 554.4 | 28.9 | 777 | 13 | AD563297 | AD563297 | Bacterial |
| 36 | 551.2 | 28.7 | 745 | 2 | AAV69757 | AAV69757 | Isopenten |
| 37 | 549.8 | 28.7 | 3183 | 6 | AAD33601 | AAD33601 | A. thalia |
| 38 | 549.2 | 28.6 | 3182 | 6 | AAD33336 | AAD33336 | A. thalia |
| 39 | 546.6 | 28.5 | 3183 | 2 | AA142919 | AA142919 | SAG12-1 p |
| 40 | 546.6 | 28.5 | 3183 | 10 | AD138701 | AD138701 | A. thalia |
| 41 | 546.6 | 28.5 | 3183 | 14 | AED64248 | AED64248 | Arabidops |
| 42 | 545.4 | 28.4 | 723 | 3 | AAD00619 | AAD00619 | Agrobacte |
| 43 | 543.6 | 28.3 | 720 | 13 | AD563266 | AD563266 | Bacterial |
| 44 | 543.6 | 28.3 | 720 | 13 | AD563290 | AD563290 | Bacterial |
| 45 | 543.6 | 28.3 | 720 | 13 | AD563262 | AD563262 | Bacterial |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | |
| ADT92127 | |
| ID | ADT92127 standard; DNA; 1919 BP. |
| XX | |
| AC | ADT92127; |
| XX | |
| DT | 13-JAN-2005 (first entry) |
| XX | |
| DE | A. tumefaciens isopentenyl transferase (ipt) encoding DNA. |
| XX | |
| KX | Ipt; transgenic; plant; cytokinin; female reproduction; |
| KM | isopentenyl transferase; plant breeding; gene; ds. |
| XX | |
| OS | Agrobacterium tumefaciens. |
| XX | |
| FH | Key |
| FT | Location/Qualifiers |
| FT | 690..1409 |
| FT | /*tag= a |
| FT | /product= "ipt" |
| XX | |
| FN | W02004090143-A2. |
| XX | |
| PD | 21-OCT-2004. |
| XX | |
| PF | 02-APR-2004; 2004WO-US010064. |
| XX | |
| PR | 04-APR-2003; 2003US-0460718P. |
| XX | |
| PA | (PTON-) PIONEER HI-BRED INT INC. |
| XX | |
| PI | Habben JE, Zinselmeyer C, Tomes DT, Abblitt SE, Helentjaris TG; |
| PI | Niu X; |
| XX | |
| DR | WPI; 2004-748771/73. |
| DR | P-PSDB; ADT92128. |
| DR | GENBANK; X14410. |
| XX | |
| PT | Producing transgenic plants capable of regulated expression of cytokinin- |
| PT | modulating gene, comprises transformation of plant cells with a genetic |
| PT | construct capable of temporally- or spatially-regulated expression of |
| PT | cytokinin modulating gene. |

XX Claim 37, SEQ ID NO 1, 157bp; English.

XX The invention relates to producing transgenic plants capable of the

CC regulated expression of a cytokinin-modulating gene in developing seed or

CC related female reproductive tissue. The method involves transformation of

CC plant host cells with a genetic construct capable of temporally- or

CC spatially-regulated expression of a cytokinin modulating gene in

CC developing seed or related female reproductive tissue, and regenerating

CC and recovering the transgenic plants. The transformation is carried out

CC by electroporation, PEG poration, particle bombardment, silicon fiber

CC delivery, microinjection, or Agrobacterium-mediated transformation. The

CC genetic construct comprises a promoter directing temporal or spatial gene

CC expression in developing seed or related female reproductive tissue,

CC operably linked to a cytokinin-modulating gene. The promoter is selected

CC from zag2.1, zap, tbi, eep1, eep2, F3.7, thxH, Zm40, ESR, PCNA2, leri1,

CC ZmCkx1-2, ZmCkx2, ZmCkx3, ZmCkx5, or ZmCkx5. The cytokinin-modulating

CC gene is selected from genes encoding cytokinin biosynthetic enzymes,

CC cytokinin catabolic enzymes, cytokinin catabolic enzyme antagonists, or

CC cytokinin biosynthetic enzyme agonists. The method is useful for

CC producing transgenic plants having enhanced cytokinin activity.

CC Transgenic plants exhibit useful characteristics including improved seed

CC size, decreased tip kernel abortion, increased seed set during

CC unfavorable environmental conditions, or stability of yield. The probes

CC that hybridize to cytokinin metabolic enzyme polynucleotide sequences are

CC useful as molecular markers in breeding programs. The inhibitors to the

CC polypeptides are useful for modulating the activity and/or expression of

CC the polypeptides. The products, compositions, processes, and methods

CC above are useful for research, biological, and agricultural purposes. The

CC present sequence represents a DNA encoding an A. tumefaciens isopentenyl

CC transferase (ipt) enzyme.

XX

SQ Sequence 1919 Bp; 533 A; 378 C; 441 G; 567 T; 0 U; 0 Other;

Query Match 100.0%; Score 1919; DB 13; Length 1919;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATCCGGTACAAAGATTTGCAAGTTTGTAAATTTGATTAATGCAATCTGGATGTTT 60

DB 1 GGATCCGGTACAAAGATTTGCAAGTTTGTAAATTTGATTAATGCAATCTGGATGTTT 60

QY 61 AATAACGAATGTANTGCGTGAAGAAATGTAATTTTATGTAATCTTCTTACATGTTG 120

DB 61 AATAACGAATGTANTGCGTGAAGAAATGTAATTTTATGTAATCTTCTTACATGTTG 120

QY 121 AAGTTTGCATATATGCTAATGTAATGTAATTAATAAATTAATGACTGCGCATTTGTTCAA 180

DB 121 AAGTTTGCATATATGCTAATGTAATGTAATTAATAAATTAATGACTGCGCATTTGTTCAA 180

QY 181 ATGCGCGCGTATTTCAAAAATATCTTTGATTGTTCAGAGCAACGACTGACGAGAG 240

DB 181 ATGCGCGCGTATTTCAAAAATATCTTTGATTGTTCAGAGCAACGACTGACGAGAG 240

QY 241 TAAATTAAGAAGCGCTGTTGTAAGAAATGCTATCATATGCGCAGCTATAGGGCAAT 300

DB 241 TAAATTAAGAAGCGCTGTTGTAAGAAATGCTATCATATGCGCAGCTATAGGGCAAT 300

QY 301 TAAATTCATATGTAAGAAATGCGCCCTTATTTTGACGCTCATCAAAATCAAAATTTTAAA 360

DB 301 TAAATTCATATGTAAGAAATGCGCCCTTATTTTGACGCTCATCAAAATCAAAATTTTAAA 360

QY 361 AATATCTCACTCTGTGCGCAGCAATGATGTAATAACGCGAGAAAAAGTGAAGTAATGCG 420

DB 361 AATATCTCACTCTGTGCGCAGCAATGATGTAATAACGCGAGAAAAAGTGAAGTAATGCG 420

QY 421 GGAAGAAAGTGGCGGAGTGGAGTAATAGCGGCTCCGCTATTCGATGTTTGTGACGTTT 480

DB 421 GGAAGAAAGTGGCGGAGTGGAGTAATAGCGGCTCCGCTATTCGATGTTTGTGACGTTT 480

QY 481 ATTGACTTAAGAGTGGCGCTGTTAGTACAAATTTGCTTTCAGAGAGACAGCCATGCC 540

DB 481 ATTGACTTAAGAGTGGCGCTGTTAGTACAAATTTGCTTTCAGAGAGACAGCCATGCC 540

QY 541 AACTTTGTTGAAAAACAAGTTGCTTTTGGGAAGAACTTAAGCACTTGCTTTCAG 600

DB 541 AACTTTGTTGAAAAACAAGTTGCTTTTGGGAAGAACTTAAGCACTTGCTTTCAG 600

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DB 601 GAGGAATATGAGAGAGAGATATTAACAGCCTGTGTACAGACTTCTTGTGCATAAAT 660

QY 661 CAATTTGATTCACATATGCGCAAGCCGATGATCTAATTTTGGTCCAACTT 720

DB 661 CAATTTGATTCACATATGCGCAAGCCGATGATCTAATTTTGGTCCAACTT 720

QY 721 GCACAGAAAGACATCACTGCGCATTACTTTCGCCAGACAGCTGGCTCCACCTCT 780

DB 721 GCACAGAAAGACATCACTGCGCATTACTTTCGCCAGACAGCTGGCTCCACCTCT 780

QY 781 CGCTCGATCGGCTCAATGCTGTCTCAACTATCAACGGAAGCGGCGCAACAGTGG 840

DB 781 CGCTCGATCGGCTCAATGCTGTCTCAACTATCAACGGAAGCGGCGCAACAGTGG 840

QY 841 AAGAATGAAAGAAAGCACTGCTGTACCTTGATGATCGCCTTTGTAAGGGTATCA 900

DB 841 AAGAATGAAAGAAAGCACTGCTGTACCTTGATGATCGCCTTTGTAAGGGTATCA 900

QY 901 TTACAGCCAGCAAGCTCAATGAAGGCTCAATGGGAGGTGCACATACAGAGGCCAAG 960

DB 901 TTACAGCCAGCAAGCTCAATGAAGGCTCAATGGGAGGTGCACATACAGAGGCCAAG 960

QY 961 GCGGCTTAATCTTGAAGAGAGATCTATCTGTTGCTCAGGTGATGGCGCAAGTCTT 1020

DB 961 GCGGCTTAATCTTGAAGAGAGATCTATCTGTTGCTCAGGTGATGGCGCAAGTCTT 1020

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DB 1021 ATTGAAACGGGATTTTCTTGGCATATTTTGCACAGAGTTAGACAGAGAGAGCT 1080

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DB 1141 TTATCCAAAGATTTGTTCAACTTTGAGAGAGCTCCGCTGAGGCCATCTGGAAGGA 1200

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DB 1201 TCGATGATATCGATATGCTCTGCTATTTGCTACCCAGAACAGATCAAGCCGATATGC 1260

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DB 1261 TATTGACGCTCGACAGCAGATATGGAAGAAATTAATGATTCACCGATATGCTCAGAGTTTC 1320

QY 1321 TAAATCCATGCGCGTGCACAGGAATTCCTTTGTGTGGGCGCAGACTGTCCAGAG 1380

DB 1321 TAAATCCATGCGCGTGCACAGGAATTCCTTTGTGTGGGCGCAGACTGTCCAGAG 1380

QY 1381 CGTTTGAAGACACCAATTTGCAATGATATGATTCACCAAGTTTGTTCAGACTTGC 1440

DB 1381 CGTTTGAAGACACCAATTTGCAATGATATGATTCACCAAGTTTGTTCAGACTTGC 1440

QY 1441 GCTATTTGATTAAGATGTTGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500

DB 1441 GCTATTTGATTAAGATGTTGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500

QY 1501 TTTGAAACTGTTTCTGCTGTTTATTTTCACTTGTGAGCAGATGTTTTCATAATATTA 1560

DB 1501 TTTGAAACTGTTTCTGCTGTTTATTTTCACTTGTGAGCAGATGTTTTCATAATATTA 1560

QY 1561 TATTGTAAAAATTTGTGTTTATTAATTCGTAGAAAGAAATTAATGTAAGTATAGCCGTTA 1620

DB 1561 TATTGTAAAAATTTGTGTTTATTAATTCGTAGAAAGAAATTAATGTAAGTATAGCCGTTA 1620


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QY 1621 TCAAAATTAGCAAAAATTGTTAAAGGTTCTTTATGCGTGAGGTTGCGACTTTTCAT 1680
DB 1621 TCAAAATTAGCAAAAATTGTTAAAGGTTCTTTATGCGTGAGGTTGCGACTTTTCAT 1680
QY 1681 CATTGTCGGTAAAGAGATTACGATATCCATACTGTAAAAACGCCGAGAAATTTACGGG 1740
DB 1681 CATTGTCGGTAAAGAGATTACGATATCCATACTGTAAAAACGCCGAGAAATTTACGGG 1740
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DB 1741 TGGTGCAATTTAGTTGGCCGTTCAACATGATTTTGGCAATAGTTGGTAACCAAGCACTAGC 1800
QY 1801 CAACCGTTGATATCACTTAATCAATGGAACCGTTCCCTTGGTGGGCTGCTC 1860
DB 1801 CAACCGTTGATATCACTTAATCAATGGAACCGTTCCCTTGGTGGGCTGCTC 1860
QY 1861 TTGATGATAGCTGCGCTGATGTTTATATACGCCGGGTTACGATTAAGACAACTT 1919
DB 1861 TTGATGATAGCTGCGCTGATGTTTATATACGCCGGGTTACGATTAAGACAACTT 1919

RESULT 2
AD055756
ID AD055756 standard; DNA; 1997 BP.
XX
AC AD055756;
XX
DT 15-JUN-2004 (first entry)
XX
DE Agrobacterium tumefaciens T-DNA [isopentenyl] transferase oncogene ipt.
XX
KW Transgenic plant; T-DNA oncogene; [isopentenyl] transferase; ipt;
KW expression cassette; tissue-preferred promoter;
KW developmental stage-preferred promoter; root growth; drought resistance;
KW seedling vigour; plant branching; gene; ds.
XX
OS Agrobacterium tumefaciens.
XX
FH Key Location/Qualifiers
FT CDS 688..1410
FT /tag= a
FT /product= "Isopentenyl transferase"
FT /EC_number= "3.5.1.27"
XX
PN WO2004000015-A2.
XX
PD 31-DEC-2003.
XX
PE 19-JUN-2003; 2003WO-US019301.
XX
PR 19-JUN-2002; 2002US-0389982P.
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Mankin SL, Da Costa E SilvaO;
XX
DR WPI; 2004-071655/07.
DR P-PSDB; AD055757.
XX
PT Improving plant performance, e.g. increased root growth, drought
PT resistance or seedling vigor comprising transforming a plant with an
PT isopentenyl transferase, a tryptophan monooxygenase or an indole
PT acetamide hydrolase.
XX
PS Claim 3; SEQ ID NO 1; 61bp; English.
XX
CC The invention relates to a method of improving plant characteristics by
CC transforming a plant with genes encoding an isopentenyl transferase (EC
CC 3.5.1.27), a tryptophan monooxygenase (EC 1.13.12.3) and/or an indole
CC acetamide hydrolase (EC 3.5.1). The method involves transforming a plant
CC cell with an expression cassette comprising an isopentenyl transferase
CC gene under the control of a tissue-preferred promoter or a developmental
CC stage-preferred promoter (but not a senescence-preferred promoter).
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CC Alternatively, the plant cell is transformed with an expression cassette
CC comprising a tryptophan monooxygenase gene and/or an indole acetamide
CC hydrolase gene operably linked to a tissue-preferred promoter. After
CC transformation, the plant cells are regenerated to form a transgenic
CC plant comprising the expression cassette. The invention also relates to
CC expression cassettes for use in the method of the invention; the
CC transgenic plants generated, and seed produced by the transgenic plants.
CC The transgenes used in the method of the invention are preferably the
CC Agrobacterium tumefaciens T-DNA oncogenes ipt (isopentenyl transferase),
CC iaam (tryptophan monooxygenase) and iaah (indole acetamide hydrolase),
CC and the tissue-preferred promoters are preferably the Arabidopsis
CC thaliana GA4H promoter or a promoter derived from an Agrobacterium
CC rhizogenes rolB promoter. The methods or the invention are useful for
CC improving the characteristics of a transgenic plant; for example, they
CC can be used to increase a plant's root growth, increase its drought
CC resistance, increase seedling vigour, or increase or decrease a plant's
CC branching. The present sequence represents the Agrobacterium tumefaciens
CC T-DNA [isopentenyl] transferase (ipt) oncogene which is specifically
CC claimed for use in the methods and expression cassettes of the invention.
XX
SQ Sequence 1997 BP; 567 A; 406 C; 441 G; 583 T; 0 U; 0 Other;
XX
Query Match 56.8%; Score 1089.8; DB 12; Length 1997;
Best Local Similarity 84.9%; Pred. No. 9.1e-269;
Matches 1270; Conservative 0; Mismatches 212; Indels 13; Gaps 4;
QY 2 GATCCGGTACAAAGTATGACAGCTTTGTAAATTCATATTAATGCAATCTGGATGTTA 61
DB 1 GATCCTGTACAAAGTATGACAGCTTTGTAAATTCATATTAATGCAATCTGGATGTTA 60
QY 62 ATTAAGAAATGTAATGGCGTA---GAAATGATATTTATATGATATTTCTTCACTAG 117
DB 61 ACMAAGAAAGTAATGGCGTAATAAGAAAAATGATATGATATGATATTTCTTCACTAG 120
QY 118 TTGAAGTTGCAATATATNGCTAATGTAATAATTAATAATGTAATGCGCGCATTTGTT 177
DB 121 TTGAAGTTGCAATATATGAT---GTAATGTAATAATGTAATGCGCGCATTTATT 174
QY 178 CAATATGGCGCGTATTTCAAAATATCTTTGATTTTGTACGAGACAAACAGCTGCAG 237
DB 175 GAAATGGCAGCTGTATTTCAACATATCTTTGATCTGTGACAAATGACAAACAGCTGCAG 234
QY 238 AAGTAAATTAAGAACGCTGTTTAAAGAAATTCATATATATGTCGCCAGCTATAGGGC 297
DB 235 AAGTAAATTAAGAACGCTGTTTAAAGAAATTCATATATGTCGCCAGCTATAGGGAC 294
QY 298 ATTTAAGTTCAATGTGAATAGCGCCCTATTATTGACGTCCTCAATCAATCAATATTTA 357
DB 295 ATTTACG-TCAATTTGTGAATATAGTCCCTTATTTTGAAGCTCTCACTTAATCAATATTTA 353
QY 358 AAAAATATCTCACTCTGTGCGCAGCAATGATGTAATAACGAGAAAAAGTAGTAAT 417
DB 354 CAACAGATCTCACTCTGTGCGCAGCAATGATGTAATGACGAGCAAAAGTAGCAATTAAG 413
QY 418 CGCGAAAAAGCTGCCGAGATGCGATGAATAGCGGCTCCGATTGCTGATTTAGTCAGC 477
DB 414 CGCGAAAAAGCTGCCGAGATGCGATGAATAGCTGCTCTGATTGCTGATTTAGTCAGC 473
QY 478 TTATATTGACTTAAGGGGCGCTGCTGTAGTGAATAATGCTTCAAGGAGACAGCATGC 537
DB 474 CTATATTGACTTAAGGGGCGCTGCTGTAGTGAATAATGCTTCAAGGAGACAGCATGC 533
QY 538 CCACACTTTGTGAAAAACAAGTTGCTTTGGGAGAAACCTAAAGCCACTTGTCTTC 597
DB 534 CCACACTGTGTGAAAAACAATTTGCTTTGGGAGAACGTAAGCAGTGTCTTC 593
QY 598 AAGAGAGAAATTCAGAGAAAGGAATATTAACGCTCTGTACAGACTTCTTGTGCAA 657
DB 594 AATAAGGAATTCAGAGAGGGAATATTAACGCTCTGTGTATACACTTCTTAATCCAA 653
QY 658 AATCAATTTGATTAACATATGCG--AAGACGATGATCTAGCTTAATTTTCGGTCC 715
DB 654 AATCAATTTGATTAACATATGCGCAAAACCTATATGATCTGCTTAATTTTCGGTCC 713
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|----|------|----------------------|---|------|
| QY | 716 | AACTTGACAAGGAAGA | CATGCACTGCGATAGCTTTGGCCAGAGACATGGCCCTCCAGT | 775 |
| Db | 714 | AACTTGACAAGGAAGA | AGCTGACCGCGGTAGCTTTGCCACAGCAGATGGGGCTTCCAGT | 773 |
| QY | 776 | CTCTCGCTCGATCGCGTCC | CAATCTGCTCTTCCAACTATCCAACTCGAAGCGGGCCACCAAC | 835 |
| Db | 774 | CCTTTCCTCGATCGGGGTCC | AAATGTGTGCTCCACTGTGCAACCGGAAGCGAGCACAAC | 833 |
| QY | 836 | AGTGAAGAAGCTGAAGA | AGCAACTGCGCTCTACCTTGATGATGAGCCCTTTGGTAAAGG | 895 |
| Db | 834 | AGTGAAGAAGCTGAAGA | AGCAAGCAGCCGCTATACCTTGATATAGCGGCTCTGGTGAAGG | 893 |
| QY | 896 | TATCATTTACAGCCCAAG | CAAGCTCATGGAACGAGCTCTTTGCGAGGTGCACATTCAGAGGC | 955 |
| Db | 894 | TATCATGCGACCCCAAG | CAAGCTCATGGAAGGCTGATGGGGAGGTGTATATTTATGAGGC | 953 |
| QY | 956 | CAAAAGCGGGCTTATCTT | TGAGGGAGGATCTATCTGTTGCTCAGGTGCATGGCGCAAG | 1015 |
| Db | 954 | CCAAGCGGGCTTATCTT | TGAGGGAGGATCTATCTGTTGCTCAAGTGCATGGCGCAAG | 1013 |
| QY | 1016 | TCGTTATTGGAACCGG | ATTTTCGTTGGCATATATTCCGAACGATTTAGACAGAGGA | 1075 |
| Db | 1014 | CAGTTATTGGAAGTCGG | ATTTTCGTTGGCATATATTCCGACAGGTTAGACAGAGGA | 1073 |
| QY | 1076 | GAGCTTCATGAGCGTGG | CCCAAGACAGAGTTTAAAGCCCTCTGACAGTCT | 1135 |
| Db | 1074 | GACCTTCATGAACTGG | CCCAAGGCCAGAGTTTAAGCAGATTTTACCCCGCTTCAGGCTT | 1133 |
| QY | 1136 | TTCTATTATCCAAAG | TTTGTTTCAACTTTGAGAGGAGCTTCGCGCTGAGGCCCATCTGGA | 1195 |
| Db | 1134 | TTCTATTATCCAAAG | TTTGTTTGAATCTTTGGAAGAGCGCTCGGCTGAGGCCCATCTGAA | 1193 |
| QY | 1196 | AGGATCGATGGATATG | ATATGCTATTTGCTATTTGCTAACCCAGAACAGATTCAGGCCGA | 1255 |
| Db | 1194 | AGATATGATGATATG | ATATGCTATTTGCTATTTGTTTGAACCAAGAACAGATTCAGTCGA | 1253 |
| QY | 1256 | TATGCTATTGAGCTCG | AGCAGAGATATGAGAAATTAATGATTCACGCTATCGCTCAGGA | 1315 |
| Db | 1254 | TATGCTATTGAGCTTGA | CGAGATATGAGAGATTAAGTTGATTCATGGGAATCGCTCAGGA | 1313 |
| QY | 1316 | GTTCCTAATCCATGCG | CGCTGCACAGGAACAGAAATTCCTTTGTTGTTGGCGCGGACAGCTGT | 1375 |
| Db | 1314 | GTATCTCATTCATGAG | CCGCCGACAAGACAGAAATTCCTCGAGTTAACGAGGCGGCTTA | 1373 |
| QY | 1376 | CGAAGCGTTTGAAGGA | CCACAATTTGCAATGTGATAGATTCGACCAAGTTTGTTTTCAAGAC | 1435 |
| Db | 1374 | CGAGCGAATTCGAAG | GTCAATTCATTCGGAATGATTAAGTTTCACACCAAGCTCCGCGTCACAC | 1433 |
| QY | 1436 | TTTGTCGATTTGGAATA | GATGTTGCTTTGTTGTTGGTGTGGTGTGTGATAG | 1490 |
| Db | 1434 | CTGTCTTCATTTGAATA | GATGTTGCGAATGTTTAAAGCTTTTAAAGCTTTTGTGTTGTGTGG | 1488 |

| RESULT | 3 |
|---------|---|
| AA50182 | |
| ID | AA50182 standard; DNA; 24596 BP. |
| XX | |
| AC | AA50182; |
| XX | |
| DT | 24-OCT-2003 (revised) |
| DT | 25-MAR-2003 (revised) |
| DT | 17-OCT-1991 (first entry) |
| XX | |
| DE | Complete nucleotide sequence of the T-DNA region of the octopine Ti |
| DE | plasmid pTi15955. |
| XX | |
| KW | Plant vector; transformation-inducing principle (TiP) gene; |
| XX | octopine Ti plasmid; ss. |
| OS | <i>Agrobacterium tumefaciens</i> ; ATCC 15955. |
| IN | EPI45338-A. |

| | |
|----|--|
| XX | 19-JUN-1985. |
| PD | |
| XX | |
| PF | 16-NOV-1984; 84EP-00307969. |
| XX | |
| PR | 18-NOV-1983; 83US-00553786. |
| XX | |
| PA | (AGRK) AGRIGENETICS RES ASSOC LTD. |
| PA | (LUBR) LUBRIZOL GENETICS INC. |
| XX | |
| PI | Barker RF, Kemp JD; |
| XX | |
| DR | WPI; 1985-148223/25. |
| XX | |
| PT | New DNA vectors contg. T-DNA sequence of octopine Ti plasmid - for |
| PT | expression in plant cells to confer desirable properties to plants and |
| PT | their cells. |
| XX | |
| XX | |
| PS | Claim 28; Fig 1; 87pp; English. |
| XX | |
| CC | The inventors claim a vector contg. a transformation-inducing principle |
| CC | (TiP) gene from Ti plasmid pTi15955. The sequence of the T-DNA of the |
| CC | octopine-type Ti plasmid has fourteen open reading frames bounded by |
| CC | eucaryotic promoters, ribosome binding sites, and polyadenylation sites. |
| CC | With the vectors, expression of structural foreign genes in plant cells |
| CC | is promoted. The gene esp. encodes an insecticidal toxin identical to or |
| CC | derived from the crystal protein of Bacillus thuringiensis. (Updated on |
| CC | 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise |
| CC | OS field) |
| XX | |
| Q0 | Sequence 24596 BP; 6534 A; 5510 C; 5793 G; 6759 T; 0 U; 0 Other; |

| Query Match | 49.9%; | Score 958.4; | DB 1; | Length 24596; |
|-----------------------|--------------|---|-----------------|---------------|
| Best Local Similarity | 81.5%; | Pred. No. 1.2e-234; | | |
| Matches 1221; | Conservative | 0; | Mismatches 261; | Indels 16; |
| | | | | Gaps 9; |
| QY | 1 | GGATCCCGCTTACAAAGTATGGACCGCTTTGGTAATGCAATTAATGCAATCTGGATGTTT | 60 | |
| Db | 8082 | GGATTCCTGTTCACAGTATTTGCAGGTTTATTAATTCATATTAAATGCAATCTTGATTTTT | 8141 | |
| QY | 61 | AATAACCAATGTAAATGGCGTGAATAATGTATTTTATGTATTTATCTTTCACATATGTTG | 120 | |
| Db | 8142 | AACACACAAACCTAATGGCGTA-AAAAATGTATGTAAATTAATTAATTAATTAATATG | 8200 | |
| QY | 121 | AAGTTGCAATTAATATGCTATGTAAATTAATAAATATATGCTACGCCGATTTGTTCAA | 180 | |
| Db | 8201 | GAGTGCCTCATTAATATGATGATTTATTAATTAATTAATTAATTAATTAATTAATTAATG | 8255 | |
| QY | 181 | ATGCGCGCGTATTTTCAA-----AAATATCTTTGATTTTGTACGAGACACGACTGCA | 235 | |
| Db | 8260 | ATGGCAGCTGTATTTTCAACCATGAATAATTTTGTATTTTTTTTACAAATTAATTAATGCA | 8319 | |
| QY | 236 | GGAATGAATTAAGAAGCGCTGTGTGAATAATGCTATCATATATGCGCCAGCTATAGG | 295 | |
| Db | 8320 | GGAATGAATTAATGAGCGCGTGTGAATAAATGCAATCATATATGCTTAATCTATAGG | 8378 | |
| QY | 296 | CCATTTAAGTCAATTGGAATATAGCGCCCTTATTTTGAAGTCTCAATCAATCAAAAT | 355 | |
| Db | 8380 | ACAATTAAGTCAA---TTGTAAATAGTCTCCCTTATTTTAAAGACTCACTAATCAAGAT | 8433 | |
| QY | 356 | TAAAAAATATCTCACTCTGTGCGCAGCAATGATATATACCGCAGAAAAGTAGAGTAA | 415 | |
| Db | 8437 | TACAAAATATCTCACT-TTTCGTGATGATATGTAATCAAGACTGATAGTACAAAGTAA | 8495 | |
| QY | 416 | ATCGCGGAAAAAGTCGCGGAGATGGCAATATACGCGCTCCGATATGCTGATTAAGTCA | 475 | |
| Db | 8496 | AACGTGAAAAAGTCATGAGTGGCAAGATTAATTTCTTGCAATGCCAATTTATTC | 8555 | |
| QY | 476 | GCTTATTTTGAAGGTGCGCTCGTTAGTGAACAAATGCTTTCAAGAGACAGCCAT | 535 | |
| Db | 8556 | GCTTATTTTGAAGGTGCGCTCGTTAGTGAACAAATGCTTTCAAGAGACAGCCAT | 8611 | |
| QY | 536 | GCCCCACATTGTGTAATAACAAGTGGCTTTTGGGAGAAGCACTTAAGCATTGGCTCT | 595 | |

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Db      8616  |||||GCCCCACCTGTTGAAAAAACAATGCGCTTTTGGG-ATACGTAAGAACCGATTGCACT 8674
Qy      596   |||||TCAAGAGAAATATCGAGAAAGAAATATTAACAGCCTCTGGT-ACAGACTTCTCTTGTGC 654
Db      8675  |||||TCAATTAATGAATTTTCAAGG-AGACAAATATTAACCGCTCTGATTAACAACTTCTCAATAT 8733
Qy      655  |||||AAAAATCAATTTGATTTCAACATATCGC--AAAGCCGATGATCTAAGCTCTAATTTTCCG 712
Db      8734  |||||AAAAATCAATTTGATTTCAATATCTGCAAAAAAACTTATGACCTGCAATCTAATTTTCCG 8793
Qy      713  |||||TCCAACTTGCAAGAGAAAGACATGACATGCCATCTCTTGCCGACAGACATGCGCTCC 772
Db      8794  |||||TCCAACTTGCAAGAGAAAGACACACGCGCATGACTCTTGCCGACAGACAGGCGCTTCC 8853
Qy      773  |||||AGTCCCTGCGCTCGATCGCGTCCCAATGCTGCTCAACTATCAACCGAAGCGGCGACAC 832
Db      8854  |||||AGTCCCTTCCGCTTGATCGGGTCCCAATGCTGCTCAACTATCAACCGAAGCGGCGACAC 8913
Qy      833  |||||AACAGTGAAGAACTGAAAGAAACGACTGCTGTGTAACCTTGATGATCGCCCTTTGGTAA 892
Db      8914  |||||AACAGTGAAGAACTGAAAGAAACGACGCGTCTTACCTGATGATCGGCGCTCTGTGTA 8973
Qy      893  |||||GCGATATCTTACAGCCAAAGCAAGCTCATGAAGCGCTCATGCGGAGGTGCAACATCAGA 952
Db      8974  |||||GCGATATCTTACAGCCAAAGCAAGCTCATGATGAGGTGATCGAGAGGTGATTAATCATGA 9033
Qy      953  |||||GGCCAAAGCGGGCTTATTTCTTGAGAGAGATCTATCTCGTTGCTCAGGTGATGAGCGCA 1012
Db      9034  |||||GGCCAAAGCGGGCTTATTTCTTGAGAGAGATCTATCTCGTTGCTCAGGTGATGAGCGCG 9093
Qy      1013  |||||AAGTCGTTATTTGAAACGCGGATTTTTCGTTGCGATATTTATTCGCAACGAGTTAGACAGA 1072
Db      9094  |||||AAACGCTATTGAGATGACAGATTTTCGTTGCGATATTTATTCGCCACAAAGTTACCGACA 9153
Qy      1073  |||||GGAGAGCTTCATGAGCGGTGCCAAGACCAAGATTAAAGAGATTTACGCCCCCTCTGACAG 1132
Db      9154  |||||AGAGACCTTCATGAAAGCGGCGCAAGGCGCAAGATTAAAGAGATTTGACACCCCGCTGCA 9213
Qy      1133  |||||TCTTCTATTTATTCGAAGATTGGTTCAACTTTGAGAGAGCGCTCGGCTGAGGCCCATCT 1192
Db      9214  |||||CCATTCTATTTATTCGAAGATTGGTTCCTTTGGAATGAACCTCGGCTGAGGCCCATCT 9273
Qy      1193  |||||GGAAGGATCGATGGAATATCGATATGCGCTGCTATTTGCTAACCCAGAACAGATCAGCGC 1252
Db      9274  |||||GAAAGATATCGATGGAATATCGATATGCGATGCTGTTGCTAGCCAGAACAGATCAGCGC 9333
Qy      1253  |||||CGATATGCTATTTGCGCTCGACGCGCATATGGAATATGAATTAATTCACGATTCAGCTCA 1312
Db      9334  |||||AGATATGCTATTTGCGCTTGAAGCAAAATATGGAAGTAAATTAATGAGATGCGTCA 9393
Qy      1313  |||||GGAATTTCTAATTCATGCGCGCTCGACAGAAACAGAAATTCCTTTGATGAGCGGCGCA 1372
Db      9394  |||||GGAATTTCTAATTCATGCGCGCTCGACAGAAACAGAAATTCCTTTGATGAGCGGCGC 9453
Qy      1373  |||||TGTGCAAGCGTTTGAAGACCAACATTTGCAATGTGATATGATGACCAAGTTTGTTC 1432
Db      9454  |||||TTTGACAGGATTCGAAGGTCATCGCTCGAAATGATATGATTAAGTACCGCAGCGCTG 9513
Qy      1433  |||||GACTTGTGCTATTTGAATTAAGATGTTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 1490
Db      9514  |||||CACCTGTCTTCATCTGGAATGAATGTTGTTATTTGCTTTGCTTGTGTGTGTGTGTGT 9571

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RESULT 4
 ID ABK12492 standard; DNA; 1988 BP.
 AC ABK12492;
 XX 18-JUN-2002 (first entry)
 DT
 XX Agrobacterium tumefaciens isopentenyl transferase (ipt) gene.

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XX      181  |||||Isopentenyl transferase; ipt; myb32; promoter; transgenic; plant;
KM      181  |||||senescence; cytokinin biosynthesis; shelf life; fruit; flower; leaf;
KM      181  |||||tuber; horticulture; carbon fixation; biomass; forage crop;
KM      181  |||||seed production; root growth; shoot growth; root formation;
KM      181  |||||apical dominance; gene; ds.
XX      181  |||||Arabidopsis thaliana.
OS      181  |||||WO200220772-A1.
XX      181  |||||14-MAR-2002.
XX      181  |||||30-AUG-2001; 2001WO-AU001092.
XX      181  |||||06-SEP-2000; 2000AU-00009946.
XX      181  |||||PR (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX      181  |||||PA (UPLT-) UNIV LA TROBE.
XX      181  |||||PA Spangenberg G, Lin YH, Parish RW, Li SF, Heazlewood J;
XX      181  |||||PI Pallaighy CK;
XX      181  |||||XX WPI; 2002-304382/34.
DR      181  |||||PT Manipulating plant senescence, useful e.g. for increasing shelf life of
PT      181  |||||fruit, comprises expressing gene involved in cytokine synthesis under
PT      181  |||||control of myb gene promoter.
XX      181  |||||BS Claim 7; Fig 2; 27pp; English.
XX      181  |||||XX The invention describes a method of manipulating senescence in a plant
CC      181  |||||comprising introducing a genetic construct that includes a myb gene
CC      181  |||||promoter linked to a gene encoding an enzyme involved in biosynthesis of
CC      181  |||||a cytokinin, where both the promoter and the gene may be used as
CC      181  |||||functionally active fragments or variants. Manipulation (specifically
CC      181  |||||delay) of senescence is used to increase shelf life of fruits, flowers,
CC      181  |||||leaves and tubers in horticultural produce and cut flowers, reduce
CC      181  |||||perishability of horticultural crops, improve carbon fixation (and thus
CC      181  |||||yield, including biomass in forage crops) and increase seed production.
CC      181  |||||Use of the myb gene promoter (unlike other promoters used for
CC      181  |||||overexpression of the cytokinin biosynthesis gene) does not cause
CC      181  |||||retarded root and shoot growth, failure of root formation, reduced apical
CC      181  |||||dominance and reduced leaf area. This sequence represents the
CC      181  |||||Agrobacterium tumefaciens isopentenyl transferase (ipt) gene, the product
CC      181  |||||of which is involved in cytokinin biosynthesis
XX      181  |||||SQ Sequence 1988 BP; 593 A; 386 C; 406 G; 603 T; 0 U; 0 Other;
Query Match 49.9%; Score 956.8; DB 6; Length 1988;
Best Local Similarity 81.4%; Pred. No. 1.2e-234;
Matches 1220; Conservative 0; Mismatches 262; Indels 16; Gaps 9;
Qy      1  |||||1 GGATCCCTTACAGTATTTGACACGTTTGTAAATGCAATTAATGAACAATCGATGTT 60
Db      1  |||||1 GGATCCCTTACAGTATTTGCAAGTTTAAATGCAATTAATGAACAATCTGATTTT 60
Qy      61  |||||61 AATAACGAATTAATGCGGTAGAAATATGATTTTATGATTTTATCTTTCATATGTTG 120
Db      61  |||||61 AATAACGAATTAATGCGGTAGCGTGA-AAAAATGATGATTTATTTATTTATTTATTTG 119
Qy      121  |||||121 AAGTTGCAATTAATGCTAAATGTAATTAATAAATTAATGATGCTGCGCATTTGTCA 180
Db      121  |||||121 AAGTTGCAATTAATGCTAAATGTAATTAATAAATTAATGATGCTGCGCATTTGTCA 180
Qy      120  |||||120 GAGTGCAGCATTAATGATGATTAATTAATTAATAA-ATTTTACTGTGACATGACTAG 178
Db      120  |||||120 GAGTGCAGCATTAATGATGATTAATTAATTAATAA-ATTTTACTGTGACATGACTAG 178
Qy      181  |||||181 ATGGCGCGGTATTTTCA-ATTTCTTTGATTTTGTAGAGAGCAACGATGCA 235
Db      179  |||||179 ATGGCAGCTTATTTCAACATGAAATTTGTGATTTTATTTTACATTAATTAATTTGCA 238
Qy      236  |||||236 GGAAGTAATTAAGACCGCTGTTGTAAGAAATGCTATCATATGCTGCGCATTAAGG 295
Db      239  |||||239 GGAAGTAATTAATGACCGCGTGTGTAATAAATTCATCATATGCTGCTATTAAGG 298

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QY 296 CCAATTAAGTTCATTTGTGAATAGCCGCTTATTTTGAAGCTCATCAATCAATAT 355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 ACAATTAAGTCMA--TTGTAATAGTCTCCCTTAATTTTAAGACTCACTTATCAAGAT 355
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 356 TAAAAATATCTCACTGTGTCCGAGCAATGATTAATTAACGCGAAAAATGAGATAA 415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 356 TACAAAATATCTCACT--TTTGTGAGTAATGATTAATCAAGACTGAATGATACAGATA 414
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 416 ATGCGGAAAAAAGCGCCGAGTGGCATGAATAGCGGCTCGGATTTGCGATTAGTCA 475
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 415 AACGTGAAAAAAGCTCATAGAGTGGCATGATTATTTCTGTGATTCCTCAATTATTTCA 474
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 476 GCTTTATTTGACTTAAGGTGCTCGTTAGTGAATAATGCTTTCAAGGAGACAGCAT 535
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 GCTTTATTTGACTTAAGGTGCTCGTTAGTGAATAATGCTTTCAAGGAGACAGCAT 534
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 536 GCCCCACACTTTGTTGAAAAACAAGTTGCCCTTTGGGAGAACCTAAAGCCACTGTGCT 595
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 GCCCCACACTTTGTTGAAAAACAAGTTGCCCTTTGGG--ATACGGTAAAGCAGTTGCACT 593
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 596 TCAAGAGGAATATCGAGAAAGATAATTAACAGCTCTGCT--ACAGACTTCTCTGTGC 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 594 TCAATTAATGAATTTCAAGG--AGACAATATAACCGCTCTGTATACACAAATTTCTAATAT 652
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 655 AAAAAATCAATTTGATTTCAATATATCG--AAGACCAATGATCTAGTCTAATTTTCCG 712
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 653 AAAAAATCAATTTGATTTCAATATATCTGAAAAAACTTATGAACTCGACCTAATTTTCCG 712
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 713 TCCAATTTGACAGAAAAAGACATCGACTGCGATAGCTTTTCCGACAGACAGTGGCTCC 772
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 713 TCCAATTTGACAGAAAAAGACAGACGCGCATAGCTTTTCCGACAGACAGAGGCTTCC 772
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 773 AGTCTCTCGCTCATGCGCTTCCAATGCTTCTCACTATCAACCGAGACGCGACAC 832
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 773 AGTCTCTCGCTCATGCGGTCCTCAATGCTTCTCACTATCAACCGAGACGCGACAC 832
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 833 AACAGTGAAGAATCGAAAGAGACGACTGCTGCTGACCTTGAATATGCGCCCTTTGTAA 892
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 833 AACAGTGAAGAATCGAAAGAGACGAGCGCTCTCACTTATGATCGGCTCTGTGTGA 892
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 893 GGGATCATCTTACAGCCAGCAAGCTCATGAACGCGCTCACTTCGAGGTGACAAATCA 952
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 893 GGGATCATCTTACAGCCAGCAAGCTCATGAGGTGATCGAGAGGTGATTAATCA 952
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 953 GGGCAAAAGCGGGCTTATTTCTTGAAGGAGATCTATCTGTTGCTCAGGTGATGGCCA 1012
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 953 GGGCAAAAGCGGGCTTATTTCTTGAAGGAGATCTCACTCTGTGTCAACTCATATGGCCG 1012
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1013 AAGTCGTTATTTGAACGCGGATTTTCTGTCATATTTTGGCAACGAGTTAGACAGAGA 1072
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1013 AAGTCGTTATTTGAACGCGGATTTTCTGTCATATTTTGGCAACGAGTTAGACAGAGA 1072
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1072 AAAACAGCTATTGAGTGAAGATTTTCTGTCATATTTTGGCAACGAGTTAGACAGAGA 1072
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1072 AAAACAGCTATTGAGTGAAGATTTTCTGTCATATTTTGGCAACGAGTTAGACAGAGA 1072
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1073 GGAGAGCTTTCATGAGCGTGGCAAGACAGAGTTAAGAGATGTTACGCCCTCTGCAGG 1132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1073 AGAAGCTTTCATGAGAGCGGCGCAAGGCGAGAGTTAAGAGATGTTGACGCCGCTGCAGG 1132
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1133 TCTTTCTAATTAATCAAGAGTTGTTCAACTTTGAGGAGCGCTCGGCTGAGGCCCACT 1192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1133 CCATTCTATTAATCAAGAGTTGTTTATCTTTGAGTAACCTCGGCTGAGGCCCACTCT 1192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1193 GGAAGGATCGATGAGATTCGATATGCGCTGTATTTGCTACCCGAAACGAGATCAGGCC 1252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1193 GAAAGAGATCGATGAGATTCGATATGCGATGTTTCTGTAGCCGAAACGAGATCAGGCC 1252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1253 CGATATGCTATTTGAGCTCGACGCGAGATATGGAATAAATGATTCAAGGTATGCTCA 1312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1253 AGATATGCTATTTGAGCTTGAAGCAAAATATGGAAGTAAAGTTGATTAATGGATGCTCA 1312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1313 GGAAGTTCTAATTCATGCGCGCTCGACAGGAAACAGAAATTTCCCTTTGGTGGCGCGACAC 1372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1313 GGAAGTTCTAATTCATGCGCGCTCGACAGGAAACAGAAATTTCCCAAGTTTAAAGCGCGC 1372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1373 TGTGAAAGCGTTTGAAGACCACTTCGAAATGTGATAGATTGACACAGTTTGTCTTCA 1432
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 1373 TTTGAGAGGATTTGAAGAGTATCCGTTGGAGATGATTAAGGATTAAGCCAGCGCTGCG 1432
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1433 GACTTGCGCTTATTTGAATTAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1490
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1433 CACCTGCTTCATCTGATTAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1490
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
AAN50226
ID AAN50226 standard; DNA; 24593 BP.
XX
AC AAN50226;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 16-OCT-1991 (first entry)
XX
DE Sequence of opine synthase gene.
XX
KW Plant vector; Ti plasmid; T-DNA; ss.
XX
OS Agrobacterium tumefaciens; Ti plasmid.
XX
PN EPl40556-A.
XX
PD 08-MAY-1985.
XX
PF 12-SEP-1984; 84EP-00306233.
XX
PR 14-SEP-1983; 83US-00532280.
XX
PA (AGRK ) AGRIGENETICS RES ASSOC LTD.
XX
PA (LUBR ) LUBRIZOL GENETICS INC.
XX
PI Dahl GA, Sutton DW, Barker RF;
XX
DR WPI; 1985-112086/19.
XX
PT Plasmid contg. opine synthase gene for selection - and foreign DNA,
PT useful as vector for transforming plant cells.
XX
PS Disclosure; Page 212-217; 69pp; Japanese.
XX
CC Plant cells (and protoplasts) and plasmids contg. the DNA fragment which
CC includes an opine synthase gene plus a gene for antibiotic resistance are
CC claimed. These plasmids provide max. efficiency for transfer of foreign
CC genes and can be amplified in the plant genome. They do not contain genes
CC specifying tumour formation and will not spread antibiotic resistance
CC throughout the plant population. (Updated on 25-MAR-2003 to correct PF
CC field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-
CC 2003 to standardise OS field)
XX
SQ Sequence 24593 BP; 6554 A; 5493 C; 5787 G; 6759 T; 0 U; 0 Other;

Query Match 49.7%; Score 953.6; DB 1; Length 24593;
Best Local Similarity 81.3%; Pred. No. 2e-233;
Matches 1218; Conservative 0; Mismatches 264; Indels 16; Gaps 9;

QY 1 GGAATCCGTTTCAAGTATTTGACAGTGTGTTGTAATTTGATTAATTAATGCAATCTGATGTT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8082 GGAATCCGTTTCAAGTATTTGACAGTGTGTTGTAATTTGATTAATTAATGCAATCTGATGTT 8141
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 AATAACGAATGAATGCGGTAGAAAATATGTAATTTTATTTATTTATCTTTCACTATGTTG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8142 AATAACGAATGAATGCGGTAGAAAATATGTAATTTTATTTATTTATTTATTTATTTATTTG 8200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 AAGTTTGAATTAATGCTATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 8201 AAGTTTGAATTAATGCTATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 8201 GAGTGCGCATTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8259
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ATGGCGCGTTTATTTCAA-----AAATATCTTTGATTTTGTAGAGAGACAAAGACTGCA 235
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 8260 ATGGCAGCTGTATTTCACCATGAAATTTTGTGATTTTTTATACATTAACAATTAATGGCA 8319
 QY 236 GGAAGTAAATTAAGACGCTGTTGTTAAGAAATGCTATCATATGTGCCAGCTATAGGG 295
 Db 8320 GGAAGTAAATTAAGACGCTGTTGTTAAGAAATGCTATCATATGTGCCAGCTATAGGG 8379
 QY 296 CCATTTAAGTCAATTGTGAATTAAGCGCGCTTATTTGACGCTCATCAATCAATAT 355
 Db 8380 ACAATTAAGTCA--TTGTAATAGTCTCCCTTATTTAAGCATCACTCAATCAAGTAT 8436
 QY 356 TAAAAAATATCTCACTCTGTCCGACGAATGATATTAACGACGAAAAAGTGAAGTAA 415
 Db 8437 TACAAAATATCTCACT-TTTGTGACGTAATGATGTAATGAACTGAATATGTAACAACTAA 8495
 QY 416 ATCGGGAAAAAGTCGCGGAGTGCATATAGCGGCTCCGTAATGCTGATTAAGTCA 475
 Db 8496 AACGTGAAAAACGTCATAGAGTGCATATATATCTCTGCAATGCGCAATTTATTCGA 8555
 QY 476 GCTTATTTGACTTAAGGGTGGCCCTGTAGTACGAATTTGCTTCAAGAGACAGCCAT 535
 Db 8556 GGTATTTGACTTAAGTGTGCTTGTGATGACAAATGCTTTCAGAGACAGCCAT 8615
 QY 536 GCCCACACTTTGTTGAAAAACAAGTGGCTTTGGGAGAGAACTTAAGCACTTGGCTCT 595
 Db 8616 GCCCACACTTTGTTGAAAAACAAGTGGCTTTGGG-ATACGGTAAAGCCAGTTGCACT 8674
 QY 596 TCAAGAGGAATATCGAGAGAGAAATATACAGCTCTGGT-ACAGACTTCTCTTGTGC 654
 Db 8675 TCAATTAATGAATTTCAAGG-AGACAAATATACCGCTCTGATTAACCAATTTCTTAATAT 8733
 QY 655 AAAAATCAATTTGTATTCACAATATCGC--AAGACGATGATCTACGCTAATTTTCCG 712
 Db 8734 AAAAATCAATTTGTATTCACAATATCTGCAAAAACTTAATGACCTGCACTTAATTTTCCG 8793
 QY 713 TCCAATTTGACAGAGAAAGACATCGACTGAGTGTGTCGACAGACAGCTGGCTGCC 772
 Db 8794 TCCAATTTGACAGAGAAAGACATCGACTGAGTGTGTCGACAGACAGCTGGCTGCC 8853
 QY 773 AGTCTCTGCTCGATCGCGTCCAAATGCTGTCTCTCAACTATCAACCGAAGCGGAGACC 832
 Db 8854 AGTCTCTGCTCGATCGCGTCCAAATGCTGTCTCTCAACTATCAACCGAAGCGGAGACC 8913
 QY 833 AAAGTGAAGAACTGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 892
 Db 8914 AAAGTGAAGAACTGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 8973
 QY 893 GGGTATCATTAAGCAAGCAAGCTCATATGAGCGCTCATTTGGGAGGTGACATATCGA 952
 Db 8974 GGGTATCATTAAGCAAGCAAGCTCATATGAGCGCTCATTTGGGAGGTGATATATCATGA 9033
 QY 953 GGCCAAAGCGGGCTTATTTCTGAGGAGAGATCTATCTCTGTTGCTCAAGGTGATGGCGCA 1012
 Db 9034 GGCCAAAGCGGGCTTATTTCTGAGGAGAGATCTATCTCTGTTGCTCAAGGTGATGGCGCG 9093
 QY 1013 AAGTGTATTTGGAACCGCGATTTTCTGTTGGCATATTTATTCGCAACGAGTTAGCAGACA 1072
 Db 9094 AAAACGCTATTTGAAGTGAAGTATTTCTGTTGAAATTTATTTCCCAAGTTAACCCGACCA 9153
 QY 1073 GGAGAGCTTCATGAGCGTGGCCCAAGACAGAGTTAAGAGAGATTAACGCGCCCTCGACGG 1132
 Db 9154 AGAGAGCTTCATGAGCGCGCCCAAGCCCAAGATTAAGAGAGATTAACGCGCGTGCAGG 9213
 QY 1133 TCTTTCTATTAATCAAGAGTTGGTCAACTTTGAGGAGAGCTCGGCTGAGGCCCATTA 1192
 Db 9214 CCATTCTATTAATTAAGAGTTGGTCAACTTTGAGATGAAGTCAAGCTCGGCTGAGGCCCATTA 9273
 QY 1193 GGAAGAGATTCATGATATTCATATGCGCTGATATTTGCTACCCGAACCATATCAAGCC 1252
 Db 9274 GAAAGAGATTCATGATATTCATATGCGATATGCGATGTTGTTCTGACCAAGAACCATATCAAGCC 9333
 QY 1253 CGATATGCTATTCAGCTCGACGAGATATGAGAGATTAATGATTCACGATATGCTCA 1312
 Db 9334 AGATATGCTATTCAGCTTCAGCGCAAAATATGAGAGATTAATGATTAATGGATGCTCA 9393

QY 1313 GGAAGTTCTAATTCATGCGCGCTGACAGGAAATTCCTTTGGTGGCGGACAGC 1372
 Db 9394 GGAAGTATTTCAATTCATGCGCGGCAAGGAAATTCCTTCAAGTTAAGCAGCGC 9453
 QY 1373 TGTGCAAGCGCTTGAAGGACCACTTCGAAATGATATGATGACCGAGTTTGTTCGA 1432
 Db 9454 TTTGCAAGCGATTCGAAAGGTCATCGTTCGAAATGATATGATGACCGAGCGCTGCTG 9513
 QY 1433 GACTTGTGCTATTTGAATTAAGATGTTGCTTTGTTGTTGTTGTTGTTGATAG 1490
 Db 9514 CACTGTCTTCACTCGAATTAAGATGTTGCTTATTTGTTGCTTTGCTGTTGCTG 9571
 RESULT 6
 AAC86511
 ID AAC86511 standard; DNA; 3017 BP.
 XX
 AC AAC86511;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.
 XX
 KW temporal gene expression; spatial gene expression; plant seed;
 KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
 KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
 KW ipt; ss.
 XX
 OS Synthetic.
 OS Zea mays.
 OS Agrobacterium tumefaciens.
 XX
 PN WO20063401-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 13-APR-2000; 2000WO-US009943.
 XX
 PR 16-APR-1999; 99US-0129844P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Haben JE, Zinselmeier C, Tomes D;
 XX
 DR WPI; 2000-672743/65.
 XX
 PT Novel recombinant DNA construct useful for producing transgenic plants
 PT having enhanced levels of cytokinin expression, improved stress tolerance
 PT and yield stability.
 XX
 PS Disclosure; Page 72-73; 76pp; English.
 XX
 CC The present sequence represents a recombinant DNA molecule of the
 CC invention. It comprises, in this order, a maize promoter, an
 CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
 CC terminator. The DNA molecules of the invention comprise a genetic
 CC construct consisting of a promoter directing temporal and/or spatial gene
 CC expression in plant seed operatively linked to a cytokinin modulating
 CC gene. The recombinant DNA molecules are useful for producing fertile,
 CC transgenic plants capable of regulated expression of a cytokinin
 CC modulating gene in developing seeds. They are also useful for improving
 CC stress tolerance and yield stability in plants. The preferential
 CC expression of recombinant DNA molecules of the invention occurs about 14-
 CC 25 days after pollination. The transgenic plants thus produced have
 CC enhanced levels of cytokinin expression exhibit improved seed size,
 CC decreased tip kernel abortion and increased seed set during unfavourable
 CC environmental conditions
 CC
 SQ Sequence 3017 BP; 865 A; 679 C; 622 G; 851 T; 0 U; 0 Other;
 Query Match 37.6%; Score 722; DB 3; Length 3017;
 Best Local Similarity 98.6%; Pred. No. 2.2e-174;

```
Matches 728; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 672 CAACATATCCGACAGCCGATGATCTACGCTAATTTTCCGTCCAACTTGACACGGAAG 731
    |||
Db 1390 CAACCCCAAGATCCCAAGATGATCTACGCTAATTTTCCGTCCAACTTGACACGGAAG 1449
QY 732 ACATCGACTGCGATGATCTTGCCACAGACCTGCGCTCCACAGCTCTGCTGATCGC 791
    |||
Db 1450 ACATCGACTGCGATGATCTTGCCACAGACCTGCGCTCCACAGCTCTGCTGATCGC 1509
QY 792 GTCCAAATGCTGCTCCTCACTATCAACCGGAGCGGGGACCAACAGTGAAGACTGAAA 851
    |||
Db 1510 GTCCAAATGCTGCTCCTCACTATCAACCGGAGCGGGGACCAACAGTGAAGACTGAAA 1569
QY 852 GGAACGACTGCTGCTACCTTGATGATCGCCCTTTGGTAAAGGGTATCATACGCCAAG 911
    |||
Db 1570 GGAACGACTGCTGCTACCTTGATGATCGCCCTTTGGTAAAGGGTATCATACGCCAAG 1629
QY 912 CAAGCTCATGAGCGGCTCATTTGGGAGGTGCAACATCAAGGCGCAAGGCGGCTTATT 971
    |||
Db 1630 CAAGCTCATGAGCGGCTCATTTGGGAGGTGCAACATCAAGGCGCAAGGCGGCTTATT 1689
QY 972 CTTCAGGAGAGATCTATCTCGTTGCTCAGGTGATGCGCAAGTCTTATTGGAACGCG 1031
    |||
Db 1690 CTTCAGGAGAGATCTATCTCGTTGCTCAGGTGATGCGCAAGTCTTATTGGAACGCG 1749
QY 1032 GATTTTGTGGCTATTTATTTCCGACGAGTTTACACAGGAGAGCTTCATGAGCTG 1091
    |||
Db 1750 GATTTTGTGGCTATTTATTTCCGACGAGTTTACACAGGAGAGCTTCATGAGCTG 1809
QY 1092 GCCAAGACCAAGATTAGCAGATGTTAGCCCTCTGAGAGTCTTTCTATTATCCAAAG 1151
    |||
Db 1810 GCCAAGACCAAGATTAGCAGATGTTAGCCCTCTGAGAGTCTTTCTATTATCCAAAG 1869
QY 1152 TTGGTTCACTTTGAGAGAGCCCTCGGCTGAGGCCATCTGAAAGGATGATGATAT 1211
    |||
Db 1870 TTGGTTCACTTTGAGAGAGCCCTCGGCTGAGGCCATCTGAAAGGATGATGATAT 1929
QY 1212 CGATATGCGCTGCTATTTTGTCAACCCAGAACGATCAAGCCCGATATGCTATTCAGACTC 1271
    |||
Db 1930 CGATATGCGCTGCTATTTTGTCAACCCAGAACGATCAAGCCCGATATGCTATTCAGACTC 1989
QY 1272 GAGCGAGATATGAGAAATTAATTGATTCACGGTATCGCTCAGAGTTTCTAATCCATGCG 1331
    |||
Db 1990 GAGCGAGATATGAGAAATTAATTGATTCACGGTATCGCTCAGAGTTTCTAATCCATGCG 2049
QY 1332 CGTGACAGGAACGAATTCCTTTGGTGGGCGCAGACGCTGTGAAAGCGTTTGAAGA 1391
    |||
Db 2050 CGTGACAGGAACGAATTCCTTTGGTGGGCGCAGACGCTGTGAAAGCGTTTGAAGA 2109
QY 1392 CCACCATTTTGAATGTGA 1409
    |||
Db 2110 CCACCATTTTGAATGTGA 2127

RESULT 7
AAC86508
ID AAC86508 standard; DNA; 2722 BP.
XX
AC AAC86508;
XX
DT 19-MAR-2001 (first entry)
XX
DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.
XX
KW temporal gene expression; spatial gene expression; plant seed;
KW cytokinin mobilizing gene; transgenic plant; seed size; stress tolerance;
KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KW ipc; ss.
XX
XX Synthetic.
OS Zea mays.
OS Agrobacterium tumefaciens.
```

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OS Solanum tuberosum.
XX
XX W0200063401-A1.
XX
XX 26-OCT-2000.
XX
XX 13-APR-2000; 2000WO-US009943.
XX
XX 16-APR-1999; 99US-0129844P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Habben JE, Zinselmeier C, Tomes D;
XX
XX WPI; 2000-672743/65.
XX
XX
XX Novel recombinant DNA construct useful for producing transgenic plants
XX having enhanced levels of cytokinin expression, improved stress tolerance
XX and yield stability.
XX
XX Disclosure; Page 70-71; 76pp; English.
XX
XX The present sequence represents a recombinant DNA molecule of the
XX invention. It comprises, in this order, a maize promoter, an
XX Agrobacterium isopentenyl transferase (ipt) gene fragment, and a Solanum
XX tuberosum terminator. The DNA molecules of the invention comprise a
XX genetic construct consisting of a promoter directing temporal and/or
XX spatial gene expression in plant seed operatively linked to a cytokinin
XX mobilizing gene. The recombinant DNA molecules are useful for producing
XX fertile, transgenic plants capable of regulated expression of a cytokinin
XX modulating gene in developing seeds. They are also useful for improving
XX stress tolerance and yield stability in plants. The preferential
XX expression of recombinant DNA molecules of the invention occurs about 14-
XX 25 days after pollination. The transgenic plants thus produced have
XX enhanced levels of cytokinin expression exhibit improved seed size,
XX decreased tip kernel abortion and increased seed set during unfavourable
XX environmental conditions
XX
XX Sequence 2722 BP; 732 A; 610 C; 619 G; 761 T; 0 U; 0 Other;
XX
XX Query Match 37.5%; Score 720.4; DB 3; Length 2722;
XX Best Local Similarity 99.9%; Pred. No. 5.5e-174;
XX Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 688 CGATGATCTACGCTAATTTTGTGCTCAACTTGCAAGAAAGACATGACGCGCTAG 747
    |||
Db 1523 CCATGATCTACGCTAATTTTGTGCTCAACTTGCAAGAAAGACATGACGCGCTAG 1582
QY 748 CTTTGGCCAGACAGTGGCTCCCACTCTGCTGATCGGCTCAATGCTGTCTC 807
    |||
Db 1583 CTTTGGCCAGACAGTGGCTCCCACTCTGCTGATCGGCTCAATGCTGTCTC 1642
QY 808 AACTATCAACCGGAAGCGGGCGACCAACAGTGAAGAACTGAAAGAACGATCTGTGT 867
    |||
Db 1643 AACTATCAACCGGAAGCGGGCGACCAACAGTGAAGAACTGAAAGAACGATCTGTGT 1702
QY 868 ACCCTGATGATCGCCCTTTGTTAAAGGTATCATTAACGCAAGCACTCAAGAGCG 927
    |||
Db 1703 ACCCTGATGATCGCCCTTTGTTAAAGGTATCATTAACGCAAGCACTCAAGAGCG 1762
QY 928 TCATTGGGAGAGTGCACAATCAAGAGCCAAAGCGGGCTTATTCTTGAGGAGATCTA 987
    |||
Db 1763 TCATTGGGAGAGTGCACAATCAAGAGCCAAAGCGGGCTTATTCTTGAGGAGATCTA 1882
QY 988 TCTGTGTTGCTCAGGTGATGCGCAAGTGTATTGAAAGCGGATTTTGTGGGATA 1047
    |||
Db 1823 TCTGTGTTGCTCAGGTGATGCGCAAGTGTATTGAAAGCGGATTTTGTGGGATA 1882
QY 1048 TTATTGCCAGAGATTGACAGAGAGAGCTTCATGACGCTGCGCAAGACGAGATTA 1107
    |||
Db 1883 TTATTGCCAGAGATTGACAGAGAGAGCTTCATGACGCTGCGCAAGACGAGATTA 1942
QY 1108 AGCAGATGTTAGCGCCCTCTGACAGGTCTTCTATTATCAAGAGTGTCTCACTTGA 1167
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DB 1943 AGCAGATGTACGCCCTCTGCAGGCTTTCTATTATCCAAAGTTGGTTCAACTTTGGA 2002
QY 1168 GGGAGCCTCGCTGAGAGCCCATCTAGAGAGGATCGATATGATATGCCCTGCTAT 1227
DB 2003 GGGAGCCTCGCTGAGAGCCCATCTAGAGAGGATCGATATGATATGCCCTGCTAT 2062
QY 1228 TTGCTAACCCAGAACGATACAGCCCGATATGCTATGAGAGCTCCAGCGATATGAGAGA 1287
DB 2063 TTGCTAACCCAGAACGATACAGCCCGATATGCTATGAGAGCTCCAGCGATATGAGAGA 2122
QY 1288 ATAAATTGATTCACGGTATCGCTCAGAGATTCTAATCCATGCGGTCGACAGGAACAGA 1347
DB 2123 ATAAATTGATTCACGGTATCGCTCAGAGATTCTAATCCATGCGGTCGACAGGAACAGA 2182
QY 1348 AATTCCTTTGGTGGGCGCGAGCAGCTGTGAAAGCGTTTGAAAGACCAACCATTTTCGATGT 1407
DB 2183 AATTCCTTTGGTGGGCGCGAGCAGCTGTGAAAGCGTTTGAAAGACCAACCATTTTCGATGT 2242
QY 1408 GA 1409
DB 2243 GA 2244

RESULT 8
AAC86507
ID AAC86507 standard; DNA; 2722 BP.
AC
XX AAC86507;
AC
XX 19-MAR-2001 (first entry)
DT
XX DNA comprising a barley promoter and Agrobacterium ipt gene.
DE
XX temporal gene expression; spatial gene expression; plant seed;
KW cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KW yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KW ipt; ss.
XX
XX Synthetic.
OS Hordeum vulgare.
OS Agrobacterium tumefaciens.
OS Zea mays.
XX
XX WO200063401-A1.
XX
XX 26-OCT-2000.
XX
XX 13-APR-2000; 2000WO-US009943.
XX
XX 16-APR-1999; 99US-0129844P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Haben JE, Zinselmeier C, Tomes D;
XX WPI; 2000-672743/65.
XX
XX Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.
XX
XX Disclosure; Page 69-70; 76pp; English.
XX
XX The present sequence represents a recombinant DNA molecule of the
CC invention. It comprises, in this order, a barley promoter, an
CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
CC terminator. The DNA molecules of the invention comprise a genetic
CC construct consisting of a promoter directing temporal and/or spatial gene
CC expression in plant seed operatively linked to a cytokinin modulating
CC gene. The recombinant DNA molecules are useful for producing fertile,
CC transgenic plants capable of regulated expression of a cytokinin
CC modulating gene in developing seeds. They are also useful for improving

CC stress tolerance and yield stability in plants. The preferential
CC expression of recombinant DNA molecules of the invention occurs about 14-
CC 25 days after pollination. The transgenic plants thus produced have
CC enhanced levels of cytokinin expression exhibit improved seed size,
CC decreased tip kernel abortion and increased seed set during unfavourable
CC environmental conditions
XX
SQ Sequence 2722 BP; 732 A; 610 C; 619 G; 761 T; 0 U; 0 Other;
Query Match 37.5%; Score 720.4; DB 3; Length 2722;
Best Local Similarity 99.9%; Pred. No. 5.5e-174;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 668 CGATGATCTACGTTCTAATTTTGGTCCAACTTGCAACGAAAGACATCGACTGCGATG 747
DB 1523 CCATGATCTACGTTCTAATTTTGGTCCAACTTGCAACGAAAGACATCGACTGCGATG 1582
QY 748 CTCTGGCCAGAGACTGGCCCTCCAGTCTCTGCTGATGCGGTCCAAATGCTGCTCTC 807
DB 1583 CTCTGGCCAGAGACTGGCCCTCCAGTCTCTGCTGATGCGGTCCAAATGCTGCTCTC 1642
QY 808 AACTATCAACCGAAGCGGCGACCAACAGTGAAGAACTGAAGAAAGAACTGCTCTCT 867
DB 1643 AACTATCAACCGAAGCGGCGACCAACAGTGAAGAACTGAAGAAAGAACTGCTCTCT 1702
QY 868 AACTATCAACCGAAGCGGCGACCAACAGTGAAGAACTGAAGAAAGAACTGCTCTCT 927
DB 1703 AACTATCAACCGAAGCGGCGACCAACAGTGAAGAACTGAAGAAAGAACTGCTCTCT 1762
QY 928 TCATTCGCGAGAGTGCACAAATACCGAGGCGAAAGCGGCTTATTTAGAGAGATCTGA 987
DB 1763 TCATTCGCGAGAGTGCACAAATACCGAGGCGAAAGCGGCTTATTTAGAGAGATCTGA 1822
QY 988 TCTCGTCTCAGAGTGCATAGCGCGCAAGTCTTATTTGGAACGCGATTTCGTTGSCATA 1047
DB 1823 TCTCGTCTCAGAGTGCATAGCGCGCAAGTCTTATTTGGAACGCGATTTCGTTGSCATA 1882
QY 1048 TTATTCGCAACGAGTTAGCAACAGAGAGAGAGCTTCATGAGCGTGGCCAAAGCAGAGTTA 1107
DB 1883 TTATTCGCAACGAGTTAGCAACAGAGAGAGAGCTTCATGAGCGTGGCCAAAGCAGAGTTA 1942
QY 1108 AGCAGATGTACGCCCCCTGACAGTCTTCTATATATCAAGATGTGTTCAACTTGA 1167
DB 1943 AGCAGATGTACGCCCCCTGACAGTCTTCTATATATCAAGATGTGTTCAACTTGA 2002
QY 1168 GGGAGCCTCGGCTGAGAGCCCATCTAGAGAGGATGATGATGATATGCCCTGCTAT 1227
DB 2003 GGGAGCCTCGGCTGAGAGCCCATCTAGAGAGGATGATGATGATATGCCCTGCTAT 2062
QY 1228 TTGCTAACCCAGAACGATACAGCCCGATATGCTATGAGAGCTCCAGCGATATGAGAGA 1287
DB 2063 TTGCTAACCCAGAACGATACAGCCCGATATGCTATGAGAGCTCCAGCGATATGAGAGA 2122
QY 1288 ATAAATTGATTCACGGTATCGCTCAGAGATTCTAATCCATGCGGTCGACAGGAACAGA 1347
DB 2123 ATAAATTGATTCACGGTATCGCTCAGAGATTCTAATCCATGCGGTCGACAGGAACAGA 2182
QY 1348 AATTCCTTTGGTGGGCGCGAGCAGCTGTGAAAGCGTTTGAAAGACCAACCATTTTCGATGT 1407
DB 2183 AATTCCTTTGGTGGGCGCGAGCAGCTGTGAAAGCGTTTGAAAGACCAACCATTTTCGATGT 2242
QY 1408 GA 1409
DB 2243 GA 2244

RESULT 9
AAC86506
ID AAC86506 standard; DNA; 5622 BP.
AC
XX AAC86506;
AC
XX 19-MAR-2001 (first entry)
DT

XX DNA construct comprising a maize promoter and Agrobacterium ipt gene.
DE
XX temporal gene expression; spatial gene expression; plant seed;
KM cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KM yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KM ipt; ss.
XX Synthetic.
OS Zea mays.
OS Agrobacterium tumefaciens.
XX W0200063401-A1.
PN
XX 26-OCT-2000.
PD
XX 13-APR-2000; 2000WO-US009943.
PF
XX 16-APR-1999; 99US-0129844P.
PR
XX (PION-) PIONEER HI-BRED INT INC.
PA
XX Habben JE, Zinselmeier C, Tomes D;
PI
XX WPI; 2000-672743/65.
DR
XX Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.
XX
PS Disclosure; Page 67-69; 76pp; English.
XX
XX The present sequence represents a recombinant DNA molecule of the
CC invention. It comprises, in this order, a maize promoter, an
CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
CC terminator. The DNA molecules of the invention comprise a genetic
CC construct consisting of a promoter directing temporal and/or spatial gene
CC expression in plant seed operatively linked to a cytokinin modulating
CC gene. The recombinant DNA molecules are useful for producing fertile,
CC transgenic plants capable of regulated expression of a cytokinin
CC modulating gene in developing seeds. They are also useful for improving
CC stress tolerance and yield stability in plants. The preferential
CC expression of recombinant DNA molecules of the invention occurs about 14-
CC 25 days after pollination. The transgenic plants thus produced have
CC enhanced levels of cytokinin expression exhibit improved seed size,
CC decreased tip kernel abortion and increased seed set during unfavourable
CC environmental conditions
CC
XX
SQ Sequence 5622 BP; 1546 A; 1295 C; 1189 G; 1592 T; 0 U; 0 Other;
Query Match 37.5%; Score 720.4; DB 3; Length 5622;
Best Local Similarity 99.9%; Pred. No. 7.3e-174;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 688 CGATGGATCTACGCTATTTTGGTCCAACTTGACAGGAAAGCATCGACTGCGATAG 747
DB 1523 CCATGGATCTACGCTATTTTGGTCCAACTTGACAGGAAAGCATCGACTGCGATAG 1552
QY 748 CTCTTGGCCAGACAGTGGCTCCAGTCTCTGCTGATCGGCTCCAACTGCTCTC 807
DB 1583 CTCTTGGCCAGACAGTGGCTCCAGTCTCTGCTGATCGGCTCCAACTGCTCTC 1642
QY 808 AACATATCAACCGGAAGCGGGGACCAACAGTGGAAAGCTGAAAGAAAGCACTGCTGT 867
DB 1643 AACATATCAACCGGAAGCGGGGACCAACAGTGGAAAGCTGAAAGAAAGCACTGCTGT 1702
QY 868 ACCTTGATGATGCGCCCTTTGGTAAAGGATCATTTACGCAAGCAAGCTCATGACGGC 927
DB 1703 ACCTTGATGATGCGCCCTTTGGTAAAGGATCATTTACGCAAGCAAGCTCATGACGGC 1762
QY 928 TCATTGGGAGAGTCACATATCAGAGGCCAAAGCGGGCTTATTTCTTGAGGAGAGATCTA 987
DB 1763 TCATTGGGAGAGTCACATATCAGAGGCCAAAGCGGGCTTATTTCTTGAGGAGAGATCTA 1822

QY 988 TCTGTGTCACAGGTGATGCGCCGAAGTGTATTGGAACGCGGATTTTGGTGATA 1047
DB 1823 TCTGTGTCACAGGTGATGCGCCGAAGTGTATTGGAACGCGGATTTTGGTGATA 1882
QY 1048 TTATTGCCAAGATTAGCAGACGAGAGAGCTTCATAGCGGTGCCAAGCAGAGTTA 1107
DB 1883 TTATTGCCAAGATTAGCAGACGAGAGAGCTTCATAGCGGTGCCAAGCAGAGTTA 1942
QY 1108 AGCAGATGTTACGCCCTCTGACAGTCTTTCTATTATTCAGAGTTGGTTCACTTTGGA 1167
DB 1943 AGCAGATGTTACGCCCTCTGACAGTCTTTCTATTATTCAGAGTTGGTTCACTTTGGA 2002
QY 1168 GGGAGCCTCGGCTGAGGCCCATTAATGGAAGGATGATGATATGATATGCTGCTAT 1227
DB 2003 GGGAGCCTCGGCTGAGGCCCATTAATGGAAGGATGATGATATGATATGCTGCTAT 2062
QY 1228 TTGCTACCCAGAACCATCATCAGCGCCGATATGCTATTGACAGCTGACAGATATGAGA 1287
DB 2063 TTGCTACCCAGAACCATCATCAGCGCCGATATGCTATTGACAGCTGACAGATATGAGA 2122
QY 1288 ATAAATTGATTACGCTATGCTCAGAGATTCTTAATTCATGCGCGTGCAGAGACAGA 1347
DB 2123 ATAAATTGATTACGCTATGCTCAGAGATTCTTAATTCATGCGCGTGCAGAGACAGA 2182
QY 1348 AATTCCTTTGCTGGGGCGACAGCTGTCCAAAGGCTTGAAGGACCAACATTTGGAATGT 1407
DB 2183 AATTCCTTTGCTGGGGCGACAGCTGTCCAAAGGCTTGAAGGACCAACATTTGGAATGT 2242
QY 1408 GA 1409
DB 2243 GA 2244
RESULT 10
ID AAC86514 standard; DNA; 721 BP.
AC AAC86514;
XX
DT 19-MAR-2001 (first entry)
XX
DE Nucleotide sequence of an isopentenyl transferase (ipt) gene fragment.
KM temporal gene expression; spatial gene expression; plant seed;
KM cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KM yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KM ipt; ss.
XX
XX Agrobacterium tumefaciens.
OS
XX W0200063401-A1.
PN
XX 26-OCT-2000.
PD
XX 13-APR-2000; 2000WO-US009943.
PF
XX 16-APR-1999; 99US-0129844P.
PR
XX (PION-) PIONEER HI-BRED INT INC.
PA
XX Habben JE, Zinselmeier C, Tomes D;
PI
XX WPI; 2000-672743/65.
DR
XX Novel recombinant DNA construct useful for producing transgenic plants
PT having enhanced levels of cytokinin expression, improved stress tolerance
PT and yield stability.
XX
PS Disclosure; Page 16; 76pp; English.
XX
XX The present sequence represents an isopentenyl transferase gene fragment.
CC The fragment was used to produce the recombinant DNA molecules of the

CC invention. These comprise a genetic construct consisting of a promoter
CC directing temporal and/or spatial gene expression in plant seed
CC operatively linked to a cytokinin modulating gene. The recombinant DNA
CC molecules are useful for producing fertile, transgenic plants capable of
CC regulated expression of a cytokinin modulating gene in developing seeds.
CC They are also useful for improving stress tolerance and yield stability
CC in plants. The preferential expression of recombinant DNA molecules of
CC the invention occurs about 14-25 days after pollination. The transgenic
CC plants thus produced have enhanced levels of cytokinin expression exhibit
CC improved seed size, decreased tip kernel abortion and increased seed set
CC during unfavourable environmental conditions

XX Sequence 721 BP; 182 A; 176 C; 191 G; 172 T; 0 U; 0 Other;

Query Match 37.5%; Score 720; DB 3; Length 721;
Best Local Similarity 100.0%; Pred. No. 4.2e-174;

Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 ATGATCTACGCTTAATTTTCGGTCCCACTTGCAAGGAAAGACATCGACTCGATAGCT 749
DB 2 ATGATCTACGCTTAATTTTCGGTCCCACTTGCAAGGAAAGACATCGACTCGATAGCT 61
QY 750 CTTGCCAGCAGACTGAGCTCCCAAGTCTCGCTCGATCGGCTCAATGCTGCTCAA 809
DB 62 CTTGCCAGCAGACTGAGCTCCCAAGTCTCGCTCGATCGGCTCAATGCTGCTCAA 121
QY 810 CTATCAACCGGAAGCGGGCGACCAACAGTGAAGAAGCTGAAGGAACGACTGCTGTAC 869
DB 122 CTATCAACCGGAAGCGGGCGACCAACAGTGAAGAAGCTGAAGGAACGACTGCTGTAC 181
QY 870 CTTGATGATCGCCCTTTGGTAAAGGGTATCATTTACAGCCACCAAGCTATGAAGGCTC 929
DB 182 CTTGATGATCGCCCTTTGGTAAAGGGTATCATTTACAGCCACCAAGCTATGAAGGCTC 241
QY 930 ATTGGGAGGTGCACATCAGAGGCGAAAGCGGGCTTATCTTGAGGAGGATCTATC 989
DB 242 ATTGGGAGGTGCACATCAGAGGCGAAAGCGGGCTTATCTTGAGGAGGATCTATC 301
QY 990 TCGTTGCTCAGGTGATGCGCGAAAGTCGTTATTGGAACGCGGATTTTCTGGCATATT 1049
DB 302 TCGTTGCTCAGGTGATGCGCGAAAGTCGTTATTGGAACGCGGATTTTCTGGCATATT 361
QY 1050 ATTGCCAAGAGTTGACGACGAGAGAGCTTCATGAGCGTGGCCAAAGCCAGATTAG 1109
DB 362 ATTGCCAAGAGTTGACGACGAGAGAGCTTCATGAGCGTGGCCAAAGCCAGATTAG 421
QY 1110 CAGATGTTACGCGCCCTCTGACAGGTCTTCTATTATCCAAAGATTGGTTCACTTTGAGG 1169
DB 422 CAGATGTTACGCGCCCTCTGACAGGTCTTCTATTATCCAAAGATTGGTTCACTTTGAGG 481
QY 1170 GAGCCTCGGCTGAGGCCCATACTGGAAGGATCGATGATATCATATGCGCTATTT 1229
DB 482 GAGCCTCGGCTGAGGCCCATACTGGAAGGATCGATGATATCATATGCGCTATTT 541
QY 1230 GCTACCCAGAACAGATCAGCGCCCATATGCTATTGTCAGCTCGACGACAGATATGAGAA 1289
DB 542 GCTACCCAGAACAGATCAGCGCCCATATGCTATTGTCAGCTCGACGACAGATATGAGAA 601
QY 1290 AAATGATTCACGAGTATGCTTCAGAGTTTCTAATCCATGCGCGTGCACAGAAACAGAA 1349
DB 602 AAATGATTCACGAGTATGCTTCAGAGTTTCTAATCCATGCGCGTGCACAGAAACAGAA 661
QY 1350 TTCCCTTTGGTGGCGGACAGCTGTCGAAGCGTTTGAAGACCAACATTTGGAATGGA 1409
DB 662 TTCCCTTTGGTGGCGGACAGCTGTCGAAGCGTTTGAAGACCAACATTTGGAATGGA 721

RESULT 11
ACF58155
ID ACF58155 standard; cDNA; 723 BP.

XX ACF58155;
XX

DT 15-JAN-2004 (first entry)

XX Z. mays isopenlenyl transferase encoding cDNA.

DE Z. mays isopenlenyl transferase; plant; transformation; transgenic; gl2; cell division;

KW isopenlenyl transferase; gene; ss.

XX Zea mays.

OS Zea mays.

XX Key Location/Qualifiers

FT CDS 1..723 /tag= a

FT /product= "isopenlenyl transferase"

XX WO2003087313-A2.

XX 23-OCT-2003.

XX 08-APR-2003; 2003WO-US010544.

XX 08-APR-2002; 2002US-0370796P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Zinselmeier C, Helentjaris TG;

XX WPI; 2003-845315/78.

XX P-PSDB; ABR61587.

PT Enhancing silk exertion in a Zea mays plant under stress, relative to a

PT non-transformed Zea mays plant under stress by transforming the plant or

PT its ancestor with a construct comprising a silk-specific or silk-

PT preferred promoter.

XX Claim 2; Page 67-68; opp; English.

XX The invention relates to enhancing silk exertion in a Zea mays plant

XX under stress, relative to a non-transformed Zea mays plant under stress.

XX The method involves transforming the plant or its ancestor with a

XX construct comprising a silk-specific or silk-preferred promoter operably

XX linked to a polynucleotide encoding a polypeptide that increases cell

XX division. The present sequence represents a cDNA encoding a Z. mays

XX isopenlenyl transferase, a polypeptide involved in cell division

XX Sequence 723 BP; 181 A; 176 C; 192 G; 174 T; 0 U; 0 Other;

Query Match 37.5%; Score 720; DB 10; Length 723;
Best Local Similarity 100.0%; Pred. No. 4.2e-174;

Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 ATGATCTACGCTTAATTTTCGGTCCCACTTGCAAGGAAAGACATCGACTCGATAGCT 749
DB 1 ATGATCTACGCTTAATTTTCGGTCCCACTTGCAAGGAAAGACATCGACTCGATAGCT 60
QY 750 CTTGCCAGCAGACTGAGCTCCCAAGTCTCGCTCGATCGGCTCAATGCTGCTCAA 809
DB 61 CTTGCCAGCAGACTGAGCTCCCAAGTCTCGCTCGATCGGCTCAATGCTGCTCAA 120
QY 810 CTATCAACCGGAAGCGGGCGACCAACATGGAAGAAGCTGAAGGAAGCAAGCTGCTGTAC 869
DB 121 CTATCAACCGGAAGCGGGCGACCAACATGGAAGAAGCTGAAGGAAGCAAGCTGCTGTAC 180
QY 870 CTTGATGATCGCCCTTTGGTAAAGGGTATCATTTACAGCCCAAGCAAGCTCATGAAGGCTC 929
DB 181 CTTGATGATCGCCCTTTGGTAAAGGGTATCATTTACAGCCCAAGCAAGCTCATGAAGGCTC 240
QY 930 ATTGGGAGGTGCACATCAGAGGCGCAAGGCGGGCTTATTTCTTGAGGAGAGATATC 989
DB 241 ATTGGGAGGTGCACATCAGAGGCGCAAGGCGGGCTTATTTCTTGAGGAGAGATATC 300
QY 990 TCGTTGCTCAGGTGATGCGCGAAAGTCGTTATTGGAACGCGGATTTTCTGGCATATT 1049
DB 301 TCGTTGCTCAGGTGATGCGCGAAAGTCGTTATTGGAACGCGGATTTTCTGGCATATT 360

QY 1050 ATTGCAACGAGTTAGCAGACGAGAGAGCTTCAATGAGCTGGCCAGACCAAGTTAAG 1109
CC ATTTGGCAACGAGTTAGCAGACGAGAGAGCTTCAATGAGCTGGCCAGACCAAGTTAAG 1109
Db 361 ATTTGGCAACGAGTTAGCAGACGAGAGAGCTTCAATGAGCTGGCCAGACCAAGTTAAG 420
QY 1110 CAGATGTTAGCCCTCTGCGAGGCTTTCTATTATTCAGAGTTGGTTCACTTTGGAGG 1169
CC CAGATGTTAGCCCTCTGCGAGGCTTTCTATTATTCAGAGTTGGTTCACTTTGGAGG 1169
Db 421 CAGATGTTAGCCCTCTGCGAGGCTTTCTATTATTCAGAGTTGGTTCACTTTGGAGG 480
QY 1170 GAGCCTGGCTGAGAGCCCATCTGGAAGGATCGATGATATGCTATGCTCTATT 1229
CC GAGCCTGGCTGAGAGCCCATCTGGAAGGATCGATGATATGCTATGCTCTATT 1229
Db 481 GAGCCTGGCTGAGAGCCCATCTGGAAGGATCGATGATATGCTATGCTCTATT 540
QY 1230 GCTACCCAGAACCAAGATCAACCCCGGATATGCTATTGCGCTGACGCGATATGAGAA 1289
CC GCTACCCAGAACCAAGATCAACCCCGGATATGCTATTGCGCTGACGCGATATGAGAA 1289
Db 541 GCTACCCAGAACCAAGATCAACCCCGGATATGCTATTGCGCTGACGCGATATGAGAA 600
QY 1290 AAATTGATTCAGGATATGCTGATGCTTCTAATTCATGCGCGTGCACAGAAACAGAA 1349
CC AAATTGATTCAGGATATGCTGATGCTTCTAATTCATGCGCGTGCACAGAAACAGAA 1349
Db 601 AAATTGATTCAGGATATGCTGATGCTTCTAATTCATGCGCGTGCACAGAAACAGAA 660
QY 1350 TTCCCTTTGGTGGGCGCAGACAGCTGTGAGAGCGTTTGAAGACCAACATTTCGAATG 1409
CC TTCCCTTTGGTGGGCGCAGACAGCTGTGAGAGCGTTTGAAGACCAACATTTCGAATG 1409
Db 661 TTCCCTTTGGTGGGCGCAGACAGCTGTGAGAGCGTTTGAAGACCAACATTTCGAATG 720

RESULT 12
ADS63261
ID ADS63261 standard; cDNA; 717 BP.
AC ADS63261;
XX 02-DEC-2004 (first entry)
XX Bacterial polynucleotide #15248.
DE
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
KM pathogen tolerance; pest tolerance; plant disease resistance;
KM cell cycle pathway modification; plant growth regulator;
KM homologous recombination; seed oil yield; protein yield; carbohydrate;
KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KM bacterial polynucleotide; gene; ss.
XX
XX Bacteria.
OS
XX US2003233675-A1.
XX
XX 18-DEC-2003.
PD
XX 20-FEB-2003; 2003US-00369493.
PF
XX 21-FEB-2002; 2002US-0360039P.
PR
XX
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 38935; 122bp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned
CC to provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. This sequence represents a bacterial polynucleotide used in
CC production. The sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
CC
XX
SQ Sequence 717 BP; 180 A; 176 C; 190 G; 171 T; 0 U; 0 Other;
Query Match 37.4%; Score 717; DB 13; Length 717;
Best Local Similarity 100.0%; Pred. No. 2.5e-173; Indels 0; Gaps 0;
Matches 717; Conservative 0; Mismatches 0;
QY 690 ATGATCTACGCTCAATTTTGGTCCAACTTGACAGAGAAAGACATGACTGCGATAGCT 749
Db 1 ATGATCTACGCTCAATTTTGGTCCAACTTGACAGAGAAAGACATGACTGCGATAGCT 60
QY 750 CTTGCCAGACAGACTGCTCCAGTCTCTGCTCGATCGCGTCCAACTGCTGCTCA 809
Db 61 CTTGCCAGACAGACTGCTCCAGTCTCTGCTCGATCGCGTCCAACTGCTGCTCA 120
QY 810 CTATCAACCCGAGACCGGCGGCAACAGTGAAGAACTGAAGAGAGAGCTGCTGAC 869
Db 121 CTATCAACCCGAGACCGGCGGCAACAGTGAAGAACTGAAGAGAGAGCTGCTGAC 180
QY 870 CTTGATGATCGCCCTTTGGTAAAGGATATCATTCAGCCAGCAAGCTCATGAACGCGCTC 929
Db 181 CTTGATGATCGCCCTTTGGTAAAGGATATCATTCAGCCAGCAAGCTCATGAACGCGCTC 240
QY 930 ATTGGGAGGTGCAATCAGACAGAGCCAGAGCGGCTTATTCTTGAGGAGATCTATC 989
Db 241 ATTGGGAGGTGCAATCAGACAGAGCCAGAGCGGCTTATTCTTGAGGAGATCTATC 300
QY 990 TCGTTGCTCAGATGCGATGCGCAAAAGCTTATGGAACGCGGATTTTGGTGGCATATT 1049
Db 301 TCGTTGCTCAGATGCGATGCGCAAAAGCTTATGGAACGCGGATTTTGGTGGCATATT 360
QY 1050 ATTGCAACGAGTTAGCAGACGAGAGAGCTTCAATGAGCTGGCCAGACCAAGTTAAG 1109
Db 361 ATTGCAACGAGTTAGCAGACGAGAGAGCTTCAATGAGCTGGCCAGACCAAGTTAAG 420
QY 1110 CAGATGTTAGCCCTCTGCGAGGCTTTCTATTATTCAGAGTTGGTTCACTTTGGAGG 1169
Db 421 CAGATGTTAGCCCTCTGCGAGGCTTTCTATTATTCAGAGTTGGTTCACTTTGGAGG 480
QY 1170 GAGCCTGGCTGAGAGCCCATCTGGAAGGATCGATGATATGCTATGCTCTATT 1229
Db 481 GAGCCTGGCTGAGAGCCCATCTGGAAGGATCGATGATATGCTATGCTCTATT 540
QY 1230 GCTACCCAGAACCAAGATCAACCCCGGATATGCTATTGCGCTGACGCGATATGAGAA 1289
Db 541 GCTACCCAGAACCAAGATCAACCCCGGATATGCTATTGCGCTGACGCGATATGAGAA 600
QY 1290 AAATTGATTCAGGATATGCTGATGCTTCTAATTCATGCGCGTGCACAGAAACAGAA 1349
Db 601 AAATTGATTCAGGATATGCTGATGCTTCTAATTCATGCGCGTGCACAGAAACAGAA 660
QY 1350 TTCCCTTTGGTGGGCGCAGACAGCTGTGAGAGCGTTTGAAGACCAACATTTCGAATG 1406

Db 661 |||||TTCCCTTGGTGGCGCGACAGCTGTGCAAGCGTTTGAAGACCAACATTTCGAATG 717
RESULT 13
ADT62691
ID ADT62691 standard; DNA; 723 BP.
XX
AC ADT62691;
XX
DT 13-JAN-2005 (first entry)
XX
DE DNA encoding A. tumefaciens isopentenyl transferase (IPT).
XX
KW DNA plasmid; transfer DNA; T-DNA; Agrobacterium Ti plasmid; transgene;
KW expression cassette; transgenic plant; transgenic;
KW isopentenyl transferase; IPT; ds.
XX
OS Agrobacterium tumefaciens.
XX
PN WO2004092390-A2.
XX
PD 28-OCT-2004.
XX
PF 09-APR-2004; 2004WO-US011000.
XX
PR 09-APR-2003; 2003US-0461459P.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Gilbertson L, Krieger E, Zhang W, Ye X;
XX
DR WPI; 2004-758349/74.
XX
PT New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid
PT first border region linked to a transgene linked to an Agrobacterium Ti
PT plasmid second border region, useful for enhancing production of
PT transgenic plants.
PS
PX Example 1; SEQ ID NO 2; 77pp; English.
XX
CC The present invention relates to a DNA plasmid comprising a transfer DNA
CC (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked
CC to at least one transgene linked to an Agrobacterium Ti plasmid second
CC border region, and located in the DNA plasmid outside of the T-DNA is a
CC plant expression cassette comprising a plant cell non-lethal negative
CC selectable marker gene linked to a vector backbone DNA. Also disclosed
CC are a method for enhancing the selection of transgenic plants that do not
CC contain vector backbone DNA, a method for reducing the copy number of a
CC transgene in a plant cell, and a transgenic plant produced by the method.
CC The DNA plasmid comprises the expression cassette comprising a promoter
CC that functions in plant cells operably linked to a plant cell non-lethal
CC negative selection marker gene. The promoter is a constitutive promoter.
CC The promoter expresses the linked non-lethal negative selection marker
CC gene product in tissue culture during plant regeneration. The plant cell
CC non-lethal negative selectable marker gene comprises a plant hormone
CC biosynthetic pathway gene, degradative gene, biosynthetic pathway
CC substrate-diverting gene or signalling gene, or metabolic interference
CC gene. The transgene is a plant positive selectable marker gene selected
CC from antibiotic resistance and herbicide resistance. The transgene
CC comprises a transgene of agronomic interest. The plant hormone
CC biosynthetic pathway gene is selected from gibberellic acid pathway
CC genes, cytokinin pathway genes, auxin pathway genes, ethylene pathway
CC genes, and abscisic acid pathway genes. The plasmid is useful for
CC enhancing the production of commercially viable transgenic plants. The
CC present sequence represents DNA encoding Agrobacterium tumefaciens
CC isopentenyl transferase (IPT) enzyme. This sequence is used as a non-
CC lethal negative selectable marker.
SQ Sequence 723 BP; 183 A; 166 C; 198 G; 176 T; 0 U; 0 Other;

Query Match 30.4%; Score 583.8; DB 13; Length 723;
Best Local Similarity 88.0%; Pred. No. 3.6e-139;

Matches 636; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
QY 690 ATGATCTACGCTTAATTTTCGGTCCAACTTGCACAGAAAGACATCGACTCGATAGCT 749
Db 1 ATGATCTCGCGCTTAATTTTCGGTCCAACTTGCACAGAAAGACATCGACTCGATAGCT 60
QY 750 CTTGCCACAGACACTGCGCTCCCACTCCTTCGCTCGATCCGGTCCAAATGCTCCTCAA 809
Db 61 CTTGCCACAGACACTGCGCTCCCACTCCTTCGCTCGATCCGGTCCAAATGCTCCTCAG 120
QY 810 CTATCAACCGAAGCGGGGCGACCAACAGTGAAGAACTGAAGAAAGCACTGCTGTAC 869
Db 121 CTGTACACCGAAGCGGGGCGACCAACAGTGAAGAACTGAAGAAAGCACTGCTGTAC 180
QY 870 CTTGATGATCGCCCTTTGGTAAAGGTATCATTTACAGCCAAAGCTTCATGACGCTC 929
Db 181 CTTGATGATCGCCCTTCGTGTGAAGGTATCATTCGACGCAACAAAGCTTCATGACGCTC 240
QY 930 ATTGCGAGGTGCACATTCACAGGCGCAAGCGGCTTATTCTTGAAGGAGATCTATC 989
Db 241 ATGGGGGAGGTGTATTAATTAATGAGCCCAAGCGGCTTATTCTTGAAGGAGATCTATC 300
QY 990 TCGTTGCTCAGGTGATGCGCGCAAGTGTATTGGAACGCGGATTTTGTGGCATATT 1049
Db 301 TCGTTGCTCAGGTGATGCGCGCAAGTGTATTGGAACGCGGATTTTGTGGCATATT 360
QY 1050 ATTGCGAAGATTAGCAGACGAGAGCTTCATGAGCGTGGCCAAAGCAGAGTTAAG 1109
Db 361 ATTGCGAAGATTAGCAGAGAGAGACTTCATGAAAGCTTCATGAAAGCTGCAAGGCGAGTTAAG 420
QY 1110 CAGATGTTACGCCCTCTGACAGGTCTTTCTATTAATTCAGAGTGTGTTCACTTTGGAGG 1169
Db 421 CAGATGTTACGCCCTCTGACAGGTCTTTCTATTAATTCAGAGTGTGTTCACTTTGGAGG 480
QY 1170 GAGCCTCGGCTGAGGCGCATCTGGAAGGATCGATGATATGATATGATGCTGCTATT 1229
Db 481 GAGCCTCGGCTGAGGCGCATCTGGAAGGATCGATGATATGATATGATGCTGCTATT 540
QY 1230 GCTACCCGAACCAAGATACGCGCGATATGCTATTGACGCTGACGAGATATGAGAA 1289
Db 541 GCTACCCGAACCAAGATACCAATCCATTCGATATGCAAGCTTGACGAGATATGAGAA 600
QY 1290 AATGATGATTCACGATATGCTTCAGAGATTTCTAATCCATGCGGCTGACAGAAACGAA 1349
Db 601 AAGTGAATTCATGAGATGCTTCAGAGATTCATTCATTCATTCATTCATTCATTCATTC 660
QY 1350 TTCCCTTGGTGGCGCGACAGCTGTGCAAGCGTTTGAAGGACCAACATTTGGAATGTA 1409
Db 661 TTCCCTGAGTTAACGACCGCTTACGACGAGATTCGAAGTCAATTCGGAATGTAT 720
QY 1410 TAG 1412
Db 721 TAG 723
RESULT 14
ADS62464
ID ADS62464 standard; cDNA; 720 BP.
XX
AC ADS62464;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polynucleotide #14451.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.

OS Bacteria.
XX US2003233675-A1.
PN 18-DEC-2003.
XX 20-FEB-2003; 2003US-00369493.
PF 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
DR
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 38138; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. Improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 720 BP; 181 A; 166 C; 198 G; 175 T; 0 U; 0 Other;
Query Match 30.4%; Score 583.6; DB 13; Length 720;
Best Local Similarity 88.3%; Pred. No. 4e-139;
Matches 634; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 690 ATGATCTACGCTTAATTTTCGGTCAACTTGACAGAAAGACATGCACTGCGATACCT 749
DB 1 ATGATCTGCGCTTAATTTTCGGTCAACTTGACAGAAAGACATGCACTGCGATACCT 60
QY 750 CTTGCCAGCAGACGCGCTCCCACTCTCTCGCTCATCGCGTCCATATGCTGTCTCAA 809
DB 61 CTTGCCAGCAGACGCGCTCCCACTCTCTCGCTCATCGCGTCCATATGCTGTCTCAG 120
QY 810 CTATCAACCGAAGGCGCGACCAACAGTGAAGAGTGAAGAGACATGCTGTGTAC 869
DB 121 CTGTCAACCGAAGGCGCGACCAACAGTGAAGAGTGAAGAGACATGCTGTGTAC 180
QY 870 CTTGATGATGCGCCCTTTGGTAAAGGGTATCATTTACAGCCAAAGCTCATGACGCGCTC 929
DB 181 CTTGATGATGCGCCCTGTGTGAAGGGTATCATTCGACCAAGCAAGCTCATGAAAGCGCTG 240

QY 930 ATTGCGAGGCTGACATTCACGAGGCCAAGCGCGGCTATTCTTGAGGAGATCTATC 989
DB 241 ATGGGGAGGTGTATTAATTATGAGGCCCGCGGCTTATTCTTGAGGAGATCTATC 300
QY 990 TCGTTGCTCAGTGCATGCGCGCAAGTCTTATTGGAACGGGATTTTCTGTGCATATT 1049
DB 301 TCGTTGCTCAAGTGCATGCGCGCAAGGCTTATTGAGTGGGATTTTCTGTGCATATT 360
QY 1050 ATTGCGACGAGTTAGCAGACGAGAGAGAGCTTATGAGCCGCGCAAGCCAGAGTTAG 1109
DB 361 ATTGCGACGAGTTAGCAGACGAGAGAGAGCTTATGAACTGGCCCAAGGTTAAG 420
QY 1110 CAGATGTTAGCGCCCTCTGACAGTCTTTCTATTATCCAGAGTGGTTCATTGAGAG 1169
DB 421 CAGATGTTAGCGCCCTCTGACAGGCTTTCTATTATCCAGAGTGGTTCATTGAGAA 480
QY 1170 GAGCCTCGGCTGAGGCCCATATCTGAAAGGATGAGATGAGATATGCTTCATTTT 1229
DB 481 GAGCCTCGGCTGAGGCCCATATCTGAAAGGATGAGATATGAGATATGCTTCATTTT 540
QY 1230 GCTTACCCAGAACCGATATCAGCCCGGATATGCTATTGTCAGCTGACGCGATATGAGAA 1289
DB 541 GCTTACCCAGAACCGATATCAGCCCGGATATGCTATTGTCAGCTGACGCGATATGAGAA 600
QY 1290 AATTTGATTCAGGATGCTCAGAGATTTCTAATTCATGCGCGTCCACAGAAACAGAA 1349
DB 601 AATTTGATTCAGGATGCTCAGAGATTTCTAATTCATGCGCGTCCACAGAAACAGAA 660
QY 1350 TTCCCTTTGGTGGCGGACAGCTGTGAAAGCGTTTGAAGACCAATTTGCAATGT 1407
DB 661 TTCCCTGAGTTAAGCAGCGCGCTTACGACGAGATTCGAAAGGTTCATTCGGAATGT 718

RESULT 15

AD559368
ID AD559368 standard; cDNA; 720 BP.

XX AC AD559368;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polynucleotide #11355.

XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polynucleotide; gene; ss.

XX OS Bacteria.

XX PN US2003233675-A1.

XX XX 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 35042; 122bp; English.

CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polynucleotide used in
CC the scope of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX

Sequence 720 BP; 181 A; 166 C; 198 G; 175 T; 0 U; 0 Other;

Query Match 30.4%; Score 583.6; DB 13; Length 720;

Best Local Similarity 88.3%; Pred. No. 4e-139;

Matches 634; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

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OY 690 ATGATCTACGCTTAATTTTGGTCCAACTTGACAGGAAAGACATCGACTGCTAGCT 749
DB 1 ATGATCTGCGCTTAATTTTGGTCCAACTTGACAGGAAAGACATCGACTGCTAGCT 60
OY 750 CTGCGCCAGACAGCTGCTCCCACTGCTCTGCTGATCGGCTCAATGCTGCTCTCA 809
DB 61 CTGCGCCAGACAGCTGCTCCCACTGCTCTGCTGATCGGCTCAATGCTGCTCTCA 120
OY 810 CTATCAACCGGAGCGGGGACCAACAGTGAAGAACTGAAGAAAGCACTGCTGTAC 869
DB 121 CTGTCACCGGAGCGGAGCAACCAAGTGAAGAACTGAAGAAAGCACTGCTGTAC 180
OY 870 CTGATGATCGGCTTTGGTAAAGGTATCATTAAGCCAAAGCAAGCTCATAGAGCTC 929
DB 181 CTGATGATCGGCTTTGGTAAAGGTATCATTAAGCCAAAGCAAGCTCATAGAGCTC 240
OY 930 ATTGGGAGGTGACATACAGAGGCAAGGCGGCTTATCTTGAGGAGGATCTATC 989
DB 241 ATTGGGAGGTGATATATATAGGCCCGGCTTATCTTGAGGAGGATCTATC 300
OY 990 TCGTGTCTCAGGTGATGCGGCAAGTCTTATTTGAAACGCGGATTTTGTGGCATAT 1049
DB 301 TCGTGTCTCAGGTGATGCGGCAAGTCTTATTTGAAAGCGGATTTTGTGGCATAT 360
OY 1050 ATTGGCAACGATTAGCAGAGAGAGCTTCATGAGGTGCGCAAGCAGAGTTAAG 1109
DB 361 ATTGGCAACGATTAGCAGAGAGAGCTTCATGAGGTGCGCAAGCAGAGTTAAG 420
OY 1110 CAGATGTTACGCGCTCTGACAGGTCTTTCTATTATTCAGAGTTGTTCACTTTGGAG 1169
DB 421 CAGATGTTACGCGCTCTGACAGGTCTTTCTATTATTCAGAGTTGTTCACTTTGGAA 480
OY 1170 GAGCTCTGAGTGGGCCCACTGAGAGGATCGATGATATCGATATGCTGCTATTT 1229
DB 481 GAGCTCTGAGTGGGCCCACTGAGAGGATCGATGATATCGATATGCTGCTATTT 540
OY 1230 GCTACCGAAGACCAATACAGCGCGGATATGCTATTTGACGCGGATATGGAAT 1289
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DB 541 GCTACCGAAGACCAATACATCCGATATGCTATTTGACGCTTGACGACGATATGAGAT 600
OY 1290 AATTTGATTACGCTATGCTTCAGAGTTTCTAATTCATGCGCGTGCACGAGAACGAAA 1349
DB 601 AAGTTGATTACGCTATGCTTCAGAGTTTCTAATTCATGCGCGGACGAGAACGAGAAA 660
OY 1350 TTCCCTTTGTTGGGGCCGACAGCTGTGGAAGGACCAACATTTTGAATGT 1407
DB 661 TTCCCTTGAGTTAACGACGCGCTTACGACGAGATTGGAAGGTCATTCATTCGGAATGT 718
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Search completed: June 26, 2006, 19:45:46
Job time : 1135 secs

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| | | | |
|----|------|---|-------|
| Db | 8142 | ATACACGACGTATGCGCTA--AAAATGTAATGTAATTAATTAATTAATTAATG | 8200 |
| Qy | 121 | AAGTTGCAATATATGCTAATGTAAATTAATAAATTAGTACTGCCGACTTTGTTCAA | 180 |
| Db | 8201 | GAGGCGCCCAATAATATGATGATTAATTAATTAATAA--TATTTACTGTCACTTACAG | 8259 |
| Qy | 181 | ATGCGCGCGTATTTTCAA-----AAATATCTTTGATTTTGTAGAGACAACACTGCA | 235 |
| Db | 8260 | ATGGCACCTGTTATTTTCAACCATGAAATTTTGTATTTTTTTTACATATACATATATGCA | 8319 |
| Qy | 236 | GGAAGTAATTAAGAAGCGCTGTGTAAAGAAATTTGTAATCATATATGTGCCACTATAGG | 295 |
| Db | 8320 | GGAAGTAATTAATATAGACGCGCTGTGTAAATAATTTGCAATCATATGTGCTTAATATAGG | 8379 |
| Qy | 296 | CCATTTTAAGTTCATATTGTAATATAGCCGCCCTTATTTTGAAGTCTCATCAATCAATAT | 355 |
| Db | 8380 | ACAAATTAAGTCAA---TTGTAATATGTCTCCCTTAATTTTAAAGACTCATCTAATCAAGAT | 8436 |
| Qy | 356 | TAAATAAATATCTACTCTGTGCGACGACATGATTAATTAACCGGACAAAGTGAAGATTA | 415 |
| Db | 8437 | TACAAATATATCTCACT--TTTGTGTAAGTAATGATTAATCAGAACTGAATATGTAAGTA | 8495 |
| Qy | 416 | ATCGCGGAAAAACGTCCGCGAGTGCATGAATAGCGGCTCCGTAATTTCTGATTTAGTCA | 475 |
| Db | 8496 | AACGTGAAAAACGTCAATAGAGTGCATGATTAATTTCTCTGCAATGCCCATAATTAATCA | 8555 |
| Qy | 476 | GCTTATTTTGCTTAAGAGGTGCCCTCGTTACTGACAAATTTCTTTCAAGAGACAGCAT | 535 |
| Db | 8556 | GCTTATTTTGCTTAAGTGTGTGCTCTTCTGTAGTGCAAATTTCTTTCAAGAGACAGCAT | 8615 |
| Qy | 536 | GCCCCACACTTTGTTAAAAACAAATGTCCTTTTGGAGAAACCTAAAGCATTGCTCT | 595 |
| Db | 8616 | GCCCCACACTTTGTTAAAAACAAATGTCCTTTTGGG--ATCGGTAAAGCCAGTTGCACT | 8674 |
| Qy | 596 | TCAAGGAGGAATATCGAGAGAGATTAATACAGCTCTGGT--ACAGCTTCTCTTGGC | 654 |
| Db | 8675 | TCAATTAAGAAATTTCAAGG--AGACATATTAACCGCTGTGAATAACAAATTTCTTAATAT | 8733 |
| Qy | 655 | AAAAATCAATTTGATTTCAACATATCGC--AAGACCGATGATCTACGTTCAATTTTCG | 712 |
| Db | 8734 | AAAAATCAATTTGATTTCAATATATCTGCMAAAAACTTATGACCTGATCTTAATTTTCG | 8793 |
| Qy | 713 | TCCAACCTTGCACAGAAAGAATGACATGACATGACTTTTCCCAAGACAGATGCGCTCCC | 772 |
| Db | 8794 | TCCAACCTTGCACAGAAAGAAGACGACCGCATATGCTTTTCCCAAGACAGAGGAGCTTCC | 8853 |
| Qy | 773 | AGTCTCTCGCTCGATCGCGTTCATATGCTGTCTCTCAACTATCAACCGGAGCGGAGCAC | 832 |
| Db | 8854 | AGTCTTTTCTGTTGATCGGATCCAAATGCTGTCTCTCACTATCAACCGGAGCGGAGCAC | 8913 |
| Qy | 833 | AACAGTGAAACCTGAAAGGAACGACTCGTCTGTACTTATGATATGCGCTTTTGTAA | 892 |
| Db | 8914 | AACAGTGAAACCTGAAAGGAACGACCGCTCTCTCACTTATGATATGCGCTCTGTGTGA | 8973 |
| Qy | 893 | GGGATATCTTACAGCAAGCAAGCTCAAGAACGCTCATTCGCTTTCGGAAGTGTGCACATTCGA | 952 |
| Db | 8974 | GGGATATCTTACAGCAAGCAAGCTCAATCAATAGGCTGATCAAGAGAGGTATTAATCATGA | 9033 |
| Qy | 953 | GGCCAAAGGCGGGCTTATCTTTGAGAGGAGATCTATCTGTTGTCTCAGTGCATATGGCGCA | 1012 |
| Db | 9034 | GGCCAACGGCGGGCTTATCTTTGAGAGGAGATTCACCTGTGTTGCAATCTCATATGGGCG | 9093 |
| Qy | 1013 | AAATGCTTATTGGAACCGCGAATTTTCGTTGGCATATTAATTTGGCAACGATTTAGCAGACGA | 1072 |
| Db | 9094 | AAACAGCTATTGAGGTGACGAATTTTCGTTGGCATATTAATTTGGCAACAAATTTACCGACCA | 9153 |
| Qy | 1073 | GGAGAGCTTACATAGAGCTGTGGCCAGACAACAGATTTAAGACAAATGTTACGCCCTCTGCAGG | 11322 |
| Db | 9154 | AGAAACCTTACATAGAAAGCGGCCAAGCCAGAGATTTAAGCAATTTTGTGACACCCCGCTGACGG | 92133 |
| Qy | 1133 | TCTTTCTATATCCAAAGTTGTTTCAAATTTTGAAGGAGCGCTCGGCTAGAGCCCATATCT | 11922 |
| Db | 9214 | CCATTTCTATATTAAGAGTTGGTTTATCTTTGGATATGAACCTCGGCTAGAGGCCCATATCT | 9273 |

[illegible]

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RESULT 2
; Sequence 12, Application US/09545334B
; Patent No. 6992237
; GENERAL INFORMATION:
; APPLICANT: Zinselemer, Chris
; APPLICANT: Habben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; TITLE OF INVENTION: Seeds
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/09/545,334B
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 3017
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Zea mays, Genbank Accession #L22344;
; OTHER INFORMATION: Gene from Agrobacterium tumefaciens. Molecular and
; OTHER INFORMATION: Genbank Accession #L22345.
; OTHER INFORMATION: Zea mays, Genbank Accession #L22345.
; US-09-545-334B-12

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|-----------------------|----------------|--|----------|-------------|
| Query Match | 37.6% | Score 722 | DB 4 | Length 3017 |
| Best Local Similarity | 98.6% | Pred. No. 2e-205 | | |
| Matches 728 | Conservative 0 | Mismatches 10 | Indels 0 | Gaps 0 |
| QY | 672 | CAACATATCGCAGACCGATGATCTACGTTAAATTTTCGGTCCAACTTGACAGGAAG | 731 | |
| Db | 1390 | CAACCCAGAGATCCACAAATGATCTCGTTAATTTTCGGTCCAACTTGACAGGAAG | 1449 | |
| QY | 732 | ACATTCGACTGGGATGAGCTCTTGCCACAGACTGGCTCCCAAGTCTCTGCTGATGCG | 791 | |
| Db | 1450 | ACATTCGACTGGGATGAGCTCTTGCCACAGACTGGCTCCCAAGTCTCTGCTGATGCG | 1509 | |
| QY | 792 | GTCCAATGCTGCTCTCAACTATCAACCGGAAGCGGGCGACCAACAGTGGAGAACTGAA | 851 | |
| Db | 1510 | GTCCAATGCTGCTCTCAACTATCAACCGGAAGCGGGCGACCAACAGTGGAGAACTGAA | 1568 | |
| QY | 852 | GGAAAGCACTGCTCTGTAACCTTGATGATGCGCCCTTTGGTAAAGGGTATCATTAACGCAAG | 911 | |
| Db | 1570 | GGAAAGCACTGCTCTGTAACCTTGATGATGCGCCCTTTGGTAAAGGGTATCATTAACGCAAG | 1629 | |
| QY | 912 | CAAGCTATGAAACGGCTCATTTGCCGAGGTGCACATCAAGAGCCAAAGCGGGCTTAT | 971 | |
| Db | 1630 | CAAGCTATGAAACGGCTCATTTGCCGAGGTGCACATCAAGAGCCAAAGCGGGCTTAT | 1688 | |

| | | | |
|---|------|--|------|
| Qy | 9712 | CTTGAAGGAGGATCTCATCTCGTTGGCTCAGAGTGCAAGGGGCAAAAGTCGTAATTGGAAAGCG | 1031 |
| Db | 1650 | CTTGAAGGAGGATCTCATCTCGTTGGCTCAGAGTGCAAGGGGCAAAAGTCGTAATTGGAAAGCG | 1749 |
| Qy | 1032 | GATTTTCGTTGGCATTTATTTTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGACGCTG | 1091 |
| Db | 1750 | GATTTTCGTTGGCATTTATTTTCGCAACGAGTTAGCAGACGAGAGAGCTTCATGACGCTG | 1809 |
| Qy | 1092 | GCCAAGACCAAGATTAAAGCAGATGTTACGCCCTCTGCAGGTCCTTTCTATTATCCAAAG | 1151 |
| Db | 1810 | GCCAAGACCAAGATTAAAGCAGATGTTACGCCCTCTGCAGGTCCTTTCTATTATCCAAAG | 1863 |
| Qy | 1152 | TTGGTTCAACTTTGGAGGAGCGTCGGCTGAGGGCCCACTAGGAAGGATGGATGGATAT | 1211 |
| Db | 1870 | TTGGTTCAACTTTGGAGGAGCGTCGGCTGAGGGCCCACTAGGAAGGATGGATGGATAT | 1923 |
| Qy | 1212 | CGATATGCCCTGCTATTTTGCTACCCAGAACCGATCAAGCCCGATATGCTATTGCAAGCTC | 1271 |
| Db | 1930 | CGATATGCCCTGCTATTTTGCTACCCAGAACCGATCAAGCCCGATATGCTATTGCAAGCTC | 1989 |
| Qy | 1272 | GACGCAAGTATGGAGAAATTAATTTGATTCACGGTATCGCTCAGAGATTTCTAATCCATGCG | 1331 |
| Db | 1990 | GACGCAAGTATGGAGAAATTAATTTGATTCACGGTATCGCTCAGAGATTTCTAATCCATGCG | 2049 |
| Qy | 1332 | CGTCGACAGGAACAGAAATTCCTCTTGGTGGGCGGACAGCGCTGTGGAAGCGTTGGAAGA | 1391 |
| Db | 2050 | CGTCGACAGGAACAGAAATTCCTCTTGGTGGGCGGACAGCGCTGTGGAAGCGTTGGAAGA | 2109 |
| Qy | 1392 | CCACCATTTCGAAATGGA | 1409 |
| Db | 2110 | CCACCATTTCGAAATGGA | 2127 |
| RESULT 3 | | | |
| US-09-545-334B-8 | | | |
| ; Sequence 8, Application US/09545334B | | | |
| ; Patent No. 6992237 | | | |
| GENERAL INFORMATION: | | | |
| APPLICANT: Zinsemeier, Chris | | | |
| APPLICANT: Habben, Jelf | | | |
| APPLICANT: Tomes, Dwight | | | |
| TITLE OF INVENTION: Regulated Expression of Genes in Plant | | | |
| TITLE OF INVENTION: Seeds | | | |
| FILE REFERENCE: 0803 | | | |
| CURRENT APPLICATION NUMBER: US/09/545,334B | | | |
| CURRENT FILING DATE: 2000-04-07 | | | |
| PRIOR APPLICATION NUMBER: US 60/129,844 | | | |
| PRIOR FILING DATE: 1999-04-16 | | | |
| NUMBER OF SEQ ID NOS: 12 | | | |
| SOFTWARE: FastSeq for Windows Version 3.0 | | | |
| SEQ ID NO 8 | | | |
| LENGTH: 2722 | | | |
| TYPE: DNA | | | |
| ORGANISM: Artificial Sequence | | | |
| FEATURE: | | | |
| OTHER INFORMATION: Promoter from Hordeum vulgare, Plant Journal 6:849-860 | | | |
| OTHER INFORMATION: (1994); gene from Agrobacterium tumefaciens, Molecular | | | |
| OTHER INFORMATION: and General Genetics 216:388-394 (1989); terminator | | | |
| OTHER INFORMATION: from Zea mays, Genbank Accession #S78780. | | | |
| US-09-545-334B-8 | | | |

| | Query Match | Similarity | Score | 720.4 | DB 4 | Length | 2722 |
|----|-------------|--|--------------|-------|--------------|--------|--------|
| | Best Local | Similarity | 99.9% | Pred. | No. 5,8e-205 | | |
| | Matches | 721 | Conservative | 0 | Mismatches | 1 | Indels |
| | | | | | | | Gaps |
| | | | | | | | 0 |
| Oy | 688 | CGATGATCTACCTCTAATTTTCGCTCCAATCTGCACAGGAAAGACATGCATCTGGATG | 747 | | | | |
| Db | 1523 | CGATGATCTACCTCTAATTTTCGCTCCAATCTGCACAGGAAAGACATGCATCTGGATG | 1582 | | | | |
| Oy | 748 | CTCTTGCCCAAGAGCTGGCCCTCCAGTCTCTGCTGCATGCGCTCCAAATGCTGTCTC | 807 | | | | |
| Db | 1583 | CTCTTGCCCAAGAGCTGGCCCTCCAGTCTCTGCTGCATGCGCTCCAAATGCTGTCTC | 1642 | | | | |

| | | | |
|----|------|--|------|
| QY | 808 | AACATCAACCCGGAAGGGGGGACCAACAGTGGAAAGAACTGGAAAGGAACGACTGCTGT | 867 |
| Db | 1643 | AACATCAACCCGGAAGGGGGGACCAACAGTGGAAAGAACTGGAAAGGAACGACTGCTGT | 1702 |
| QY | 868 | ACCTTGATGATCGCCCTTGTGGTAAAGGGTATCATTTACAGCCCAAGCCTCATAGCGC | 927 |
| Db | 1703 | ACCTTGATGATCGCCCTTGTGGTAAAGGGTATCATTTACAGCCCAAGCCTCATAGCGC | 1762 |
| QY | 928 | TCATTTGGGAGGTGCACATTCACAGAGGCCAAAGCGGGCTTATTTCTTGAGGAGAGATCTA | 987 |
| Db | 1763 | TCATTTGGGAGGTGCACAAATCACAGAGCCAAAGCGGGCTTATTTCTTGAGGAGAGATCTA | 1822 |
| QY | 988 | TCTGTGGTGCAGGTGTCATGGACGCAAGTGGTATTTGGAACGCGGATTTTCGTTGCACATA | 1047 |
| Db | 1823 | TCTGTGGTGCAGGTGTCATGGACGCAAGTGGTATTTGGAACGCGGATTTTCGTTGCACATA | 1882 |
| QY | 1048 | TTATTTCCGAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGTGGCCCAAGCCAGAGTTA | 1107 |
| Db | 1883 | TTATTTCCGAACGAGTTAGCAGACGAGAGAGCTTCATGAGCGTGGCCCAAGCCAGAGTTA | 1942 |
| QY | 1108 | AGCAGATGTTAAGCGCCCTCTGCAGAGTCTTTCATATTCGAAGATGTGTTCAATTTGGA | 1167 |
| Db | 1943 | AGCAGATGTTAAGCGCCCTCTGCAGAGTCTTTCATATTCGAAGATGTGTTCAATTTGGA | 2002 |
| QY | 1168 | GGAAGCCTCGGCTGAGGCCCATATCTGGAAGGGATCGATGATATGATATGCTCCCTGCTAT | 1227 |
| Db | 2003 | GGAAGCCTCGGCTGAGGCCCATATCTGGAAGGGATCGATGATATGATATGCTCCCTGCTAT | 2062 |
| QY | 1228 | TTGCTATCCCGAACCAGATCAACGCCCGCATATGCTATTTGCACTGCAGCGCAGATATGAGA | 1287 |
| Db | 2063 | TTGCTATCCCGAACCAGATCAACGCCCGCATATGCTATTTGCACTGCAGCGCAGATATGAGA | 2122 |
| QY | 1288 | ATTAATGATTCACAGATGCGCTCAGGAGTTTCAATCCATGCGCGTGCACAGAACAGA | 1347 |
| Db | 2123 | ATTAATGATTCACAGATGCGCTCAGGAGTTTCAATCCATGCGCGTGCACAGAACAGA | 2182 |
| QY | 1348 | AATTCCTTTGTTGGTGGCGGACAGACTGTGCAAGCGTTTGAAGGACCAACATTTGGAATGT | 1407 |
| Db | 2183 | AATTCCTTTGTTGGTGGCGGACAGACTGTGCAAGCGTTTGAAGGACCAACATTTGGAATGT | 2242 |
| QY | 1408 | GA 1409 | |
| Db | 2243 | GA 2244 | |

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RESULT 4
US-09-545-334B-9
; Sequence 9, Application US/09545334B
; Patent No. 6992237
; GENERAL INFORMATION:
; APPLICANT: Zinselmeier, Chris
; APPLICANT: Habben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; TITLE OF INVENTION: Seeds
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/09/545,334B
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter from Zea mays, U.S. patent application 09/377,648
; OTHER INFORMATION: gene from Agrobacterium tumefaciens, Molecular and General
; OTHER INFORMATION: Genetics 216:368-394 (1989); terminator from Solanum
; OTHER INFORMATION: tuberosum, Plant Cell 1(1):115-122 (1989).
US-09-545-334B-9

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| | | | | | | |
|--|---|-----------------|---------------------|-----------|--------------|--|
| | Query Match | 37.5%; | Score 720.4; | DB 4; | Length 2722; | |
| | Best Local Similarity | 99.9%; | Pred. No. 5.8e-205; | | | |
| | Matches 721; | Conservative 0; | Mismatches 1; | Indels 0; | Gaps 0; | |
| QY | 688 CGATGATCTACGTCTAATTTTGGCTCCAACTTGSCACAGGAACAATCGACTGCATAG | 747 | | | | |
| Db | 1523 CCATGATCTACGTCTAATTTTCGGTCCAACTTGSCACAGGAACAATCGACTGCATAG | 1582 | | | | |
| QY | 748 CTTCTGGCCAGCAGACATGGCCCTCCAGTCCCTGCTCGATCGGGTCCAAGCTGCTCTC | 807 | | | | |
| Db | 1583 CTTCTGGCCAGCAGACATGGCCCTCCAGTCCCTGCTCGATCGGGTCCAAGCTGCTCTC | 1642 | | | | |
| QY | 808 AACTCATCAACCGGAAGCGGGCGAACCAACAGTGAAGAATCTGAAGAACAAGCTGCTGT | 867 | | | | |
| Db | 1643 AACATCATCAACCGGAAGCGGGCGAACCAACAGTGAAGAATCTGAAGAACAAGCTGCTGT | 1702 | | | | |
| QY | 868 ACCTTGATGATCGCCCTTTGGTAAGGGTATCATTTACGCCACGAAGCTCATGAACGGC | 927 | | | | |
| Db | 1703 ACCTTGATGATCGCCCTTTGGTAAGGGTATCATTTACGCCACGAAGCTCATGAACGGC | 1762 | | | | |
| QY | 928 TCATTGGGAGAGTSCACATACGAGCGCAAGGCGGGCTTAATCTTGAGGAAGATCTA | 987 | | | | |
| Db | 1763 TCATTGGGAGAGTSCACATACGAGCGCAAGGCGGGCTTAATCTTGAGGAAGATCTA | 1822 | | | | |
| QY | 988 TCTCGTTGCTCAGGTGCATGCGGCAAGTCGTTATTGGAACGCGGATTTTTCGTTGCATYA | 1047 | | | | |
| Db | 1823 TCTCGTTGCTCAGGTGCATGCGGCAAGTCGTTATTGGAACGCGGATTTTTCGTTGCATYA | 1882 | | | | |
| Db | 1048 TTATTCCGACAGATTTAGCAGACGAGACCTTCATGACGTTGGA | 1107 | | | | |
| QY | 1048 AGCAGATGTTACGGCCCTCTGACGGTCTTTCTAATTATCAGAAGTGGTTCAACTTTGGA | 1167 | | | | |
| Db | 1943 AGCAGATGTTACGGCCCTCTGACGGTCTTTCTAATTATCAGAAGTGGTTCAACTTTGGA | 2002 | | | | |
| QY | 1168 GGGAGCCTCGGCTGAGGCCCCATACTGGAAGGATCGATGATTCGATATGCCCTGCTAT | 1227 | | | | |
| Db | 2003 GGGAGCCTCGGCTGAGGCCCCATACTGGAAGGATCGATGATTCGATATGCCCTGCTAT | 2062 | | | | |
| QY | 1228 TTGCTACCAGAACCAATGATCACGCCCCATATGCTAATTGCACTGACGCAATATGAGA | 1287 | | | | |
| Db | 2063 TTGCTACCAGAACCAATGATCACGCCCCATATGCTAATTGCACTGACGCAATATGAGA | 2122 | | | | |
| QY | 1288 ATTAATGATTCACGGTATCGCTCAGAGGTTCTTAATCCATGCGCGGTGACAGGAACAGA | 1347 | | | | |
| Db | 2123 ATTAATGATTCACGGTATCGCTCAGAGGTTCTTAATCCATGCGCGGTGACAGGAACAGA | 2182 | | | | |
| QY | 1348 AATTCCCTTTGGTGGCGCGACAGCTGTGGAAGCGTTTGAAGACCAACATTTGGAATGT | 1407 | | | | |
| Db | 2183 AATTCCCTTTGGTGGCGCGACAGCTGTGGAAGCGTTTGAAGACCAACATTTGGAATGT | 2242 | | | | |
| QY | 1408 GA 1409 | | | | | |
| Db | 2243 GA 2244 | | | | | |
| RESULT 5 | | | | | | |
| US-09-545-334B-7 | | | | | | |
| Sequence 7, Application US/09545334B | | | | | | |
| Patent No. 6992237 | | | | | | |
| GENERAL INFORMATION: | | | | | | |
| APPLICANT: Zinselmeyer, Chris | | | | | | |
| APPLICANT: Haben, Jeff | | | | | | |
| APPLICANT: Tomes, Dwight | | | | | | |
| TITLE OF INVENTION: Regulated Expression of Genes in Plant | | | | | | |
| FILE REFERENCE: 0803 | | | | | | |
| CURRENT APPLICATION NUMBER: US/09/545.334B | | | | | | |
| CURRENT FILING DATE: 2000-04-07 | | | | | | |
| PRIOR APPLICATION NUMBER: US 60/129,844 | | | | | | |
| PRIOR FILING DATE: 1999-04-16 | | | | | | |

| Query Match | 37.5% | Score 720.4 | DB 4 | Length 5622 |
|--|--------------|--|--------------|-------------|
| Best Local Similarity | 99.9% | Pred. No. 8.7e-205 | | |
| Matches 721 | Conservative | 0 | Mismatches 1 | Indels 0 |
| | | | Gaps 0 | |
| NUMBER OF SEQ ID NOS: 12 SOFTWARE: FastSeq for Windows Version 3.0 SEQ ID NO 7 LENGTH: 5622 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Promoter and terminator from Zea mays as found in OTHER INFORMATION: Genbank Accession #578780; gene from Agrobacterium OTHER INFORMATION: tumefaciens as found in Molecular and General OTHER INFORMATION: Genetics 216:388-394 (1989). US-09-545-334B-7 | | | | |
| QY | 688 | CGATGATCTACGCTCTAATTTTGGGTCCAACTTGCAAGGAAAGACATCGACTGCATAG | 747 | |
| Db | 1523 | CGATGATCTACGCTCTAATTTTGGGTCCAACTTGCAAGGAAAGACATCGACTGCATAG | 1582 | |
| QY | 748 | CTCTTGCCCAAGCACTGGCCCTCCAGTCTCTGCTGCATTCGGTCCAAATGCTGTCTC | 807 | |
| Db | 1583 | CTCTTGCCCAAGCACTGGCCCTCCAGTCTCTGCTGCATTCGGTCCAAATGCTGTCTC | 1642 | |
| QY | 808 | AACATCAACCGGAAGGGGGGACCAACAGTGGAAAGAACTGAAAGAAAGCACTGCTGT | 867 | |
| Db | 1643 | AACATCAACCGGAAGGGGGGACCAACAGTGGAAAGAACTGAAAGAAAGCACTGCTGT | 1702 | |
| QY | 868 | ACCTTGATGATCCGCTTTGGTAAAGGATTCATATCAGCCAAAGCACTCATGAAACGC | 927 | |
| Db | 1703 | ACCTTGATGATCCGCTTTGGTAAAGGATTCATATCAGCCAAAGCACTCATGAAACGC | 1762 | |
| QY | 928 | TCATTCGCGAGGTGCACATTCACAGAGCCAAAGGCGGCTTATTTCTTGAGGAGATCTA | 987 | |
| Db | 1763 | TCATTCGCGAGGTGCACATTCACAGAGCCAAAGGCGGCTTATTTCTTGAGGAGATCTA | 1822 | |
| QY | 988 | TTCTGTTGCTCAGGTGATGGCGGAAGTGTTATTTGAAACGCGGATTTTCTGTTGGGATA | 1047 | |
| Db | 1823 | TTCTGTTGCTCAGGTGATGGCGGAAGTGTTATTTGAAACGCGGATTTTCTGTTGGGATA | 1882 | |
| QY | 1048 | TTATTCGCAACGAGTTAGCAGACGAGGAGACTTCATAGACGTTGGCCCAAGCCAGAGTTA | 1107 | |
| Db | 1883 | TTATTCGCAACGAGTTAGCAGACGAGGAGACTTCATAGACGTTGGCCCAAGCCAGAGTTA | 1942 | |
| QY | 1108 | AGCAGATGTTACGCCCCCTCTGACAGTCTTCTATTTATTCACAGAGTTGTTCACTTTGGA | 1167 | |
| Db | 1943 | AGCAGATGTTACGCCCCCTCTGACAGTCTTCTATTTATTCACAGAGTTGTTCACTTTGGA | 2002 | |
| QY | 1168 | GGGAGCTTCGGCTGAGGCCCATCTGGAAGGATTCATATGATATTCATATGCTTGCCTAT | 1227 | |
| Db | 2003 | GGGAGCTTCGGCTGAGGCCCATCTGGAAGGATTCATATGATATTCATATGCTTGCCTAT | 2062 | |
| QY | 1228 | TTGCTACCCAGAACCAATGACGCGCCGATATGCTATTTGACAGCTGACGACATTTGAGA | 1287 | |
| Db | 2063 | TTGCTACCCAGAACCAATGACGCGCCGATATGCTATTTGACAGCTGACGACATTTGAGA | 2122 | |
| QY | 1288 | ATAAATGATTCAACGATATCGCTCAGAGATTCTTAATTCATGCGCTGCACAGAACAGA | 1347 | |
| Db | 2123 | ATAAATGATTCAACGATATCGCTCAGAGATTCTTAATTCATGCGCTGCACAGAACAGA | 2182 | |
| QY | 1348 | AATTCCTTTGGTGGGGCGACAGCTGTCGAAGGTTTGAAGACCAACATTTGGAATGT | 1407 | |
| Db | 2183 | AATTCCTTTGGTGGGGCGACAGCTGTCGAAGGTTTGAAGACCAACATTTGGAATGT | 2242 | |
| QY | 1408 | GA 1409 | | |
| Db | 2243 | GA 2244 | | |

Patent No. 6268552
GENERAL INFORMATION:
APPLICANT: LI, YI
TITLE OF INVENTION: Transgenic Seedless Plants
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,587
FILING DATE: 06-MAY-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,725
FILING DATE: 06-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Feider, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 4-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 745 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..725
US-09-073-587-4

Query Match 28.7%; Score 551.2; DB 3; Length 745;
Best Local Similarity 84.1%; Pred. No. 1.5e-154;
Matches 622; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 688 CGATGATCTACGCTTAATTTTGGTCCAACTTGACACAGAAAGACATCGACTGGGATAG 747
DB 1 CCATGAGACTGATCTAAATTTTGGTCCAACTTGACACAGAAAGACGACCGGATAG 60
QY 748 CTCTTGCCAGAGAGCTGCCCTCCAGTCCCTGCTGATGAGTGGCTCCAACTGCTCTC 807
DB 61 CTCTTGCCAGAGAGCTGCCCTCCAGTCCCTGCTGATGAGTGGCTCCAACTGCTCTC 120
QY 808 AACTATCAACCGGAGCGGCGACCAACAGTGAAGAACTGAAGAAAGAACTGCTGCT 867
DB 121 AACTATCAACCGGAGCGGCGACCAACAGTGAAGAACTGAAGAAAGAAAGAACTGCT 180
QY 868 ACCTTGATGATGCGCCCTTTGGTAAAGGATCATTAACAGCCAGCAAGCTCATGAAGCGC 927
DB 181 ACCTTGATGATGCGCCCTTTGGTAAAGGATCATTAACAGCCAGCAAGCTCATGAAGCGC 240
QY 928 TCATGGGAGAGGTGACAACTACGAGCGCAAGGGGCTTATTTAGGAGAGATCTA 987
DB 241 TGATGAGAGAGGTGATTAATCATGTAGGCCCAACGCGGCTTATTTAGGAGAGATCTCA 300
QY 988 TCTCGTCTCAAGTGCATGAGCGCAAGTCTTATTTGAACGCGGATTTTCGTTGGCATTA 1047
DB 301 CCTGTTCTCAACAGTGCATGAGCGCAAGTCTTATTTGAAGTGCATTTTCGTTGGCATTA 360

QY 1048 TTATTCGACAGAGTTAGCAGACGAGAGACTTCATAGCGGTGSCCAAGCCAGAGTTA 1107
DB 361 TTATTCGACAGAGTTAGCAGACGAGAGACTTCATAGAAAGCGGCCAAGCCAGAGTTA 420
QY 1108 AGCAGATGTTAGCGCCCTCTGACAGGTCTTTCTAATATCCAAAGTGTGTTCACTTTGA 1167
DB 421 AGCAGATGTTAGCGCCCTCTGACAGGTCTTTCTAATATCCAAAGTGTGTTCACTTTGA 480
QY 1168 GGGAGCCTCGGCTGAGGCCCATCTAGAAAGGATGATGATGATATGATGCTGCTAT 1227
DB 481 ATGAACCTCGGCTGAGGCCCATCTAGAAAGGATGATGATGATGATGATGCTGCTAT 540
QY 1228 TTGCTACCCAGAACCAATGACGCCCATATGCTATTGCACTGACGCAATATAGAGA 1287
DB 541 TTGCTACCCAGAACCAATGACGCCCATATGCTATTGCACTGACGCAATATAGAGA 600
QY 1288 ATAAATGATTCACGGTATGCTGCTGACAGGTTCTTAATCATGCGGCGTGAACAGAGA 1347
DB 601 GTAGTTATTAATGAGATCGCTCAGAGTATTTTCATCATATCGCGCCAAACAGAAACGA 660
QY 1348 AATTCCTTTGATGAGCGCGACAGCTGTGGAAGCGTTGGAAGAACCAACATTTGAAATG 1407
DB 661 AATTCCTTTGATGAGCGCGACAGCTGTGGAAGCGTTGGAAGAACCAACATTTGAAATG 720
QY 1408 GATGATTCACACCACTTTTG 1427
DB 721 ATTAGTTACGCGACGCCCTG 740

RESULT 7
US-08-971-395-1
Sequence 1, Application US/08971395
Patent No. 6359197

GENERAL INFORMATION:
APPLICANT: Amasino, Richard M
APPLICANT: No. 6359197, Yoo-Sun
APPLICANT: Gan, Susheng
TITLE OF INVENTION: Transgenic Plants with Altered
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,395
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.94908
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-971-395-1

Query Match 28.6%; Score 549.2; DB 3; Length 3182;

Best Local Similarity 83.5%; Pred. No. 1.3e-153;
Matches 623; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

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QY 682 CAAGACCGATGATCTACGCTTAATTTTCGCTCCAACTTGACAGAAAGACATGACTG 741
Db 2173 CTAAACCACTGACCTGCATCTAATTTTCGCTCCAACTTGACAGAAAGACAGACCG 2232
QY 742 CGATAGCTCTTGCCAGACAGCTGCTCCAGTCTCTGCTCGATCGCTCCAACTGCT 801
Db 2233 CGATAGCTCTTGCCAGACAGCTGCTCCAGTCTCTGCTCGATCGCTCCAACTGCT 2292
QY 802 GTCTCTCACTATCAACCGGAAAGCGGAGCAACCAAGTGAAGAACTGAAGAGAAAGCACTC 861
Db 2293 GTCTCTCACTATCAACCGGAAAGCGGAGCAACCAAGTGAAGAACTGAAGAGAAAGCACTC 2352
QY 862 GTCTCTCACTATGATGATGCTGCTCTTGTGAAGGATCATTAACAGCAAGCAAGCTCATG 921
Db 2353 GTCTCTCACTATGATGATGCTGCTCTTGTGAAGGATCATTAACAGCAAGCAAGCTCATG 2412
QY 922 AACGGCTCATTTGCGAGGTGCACAATCAACGAGGCCAAAGCGGCTTATTTTGAAGGAG 981
Db 2413 ATAGGCTCATTTGCGAGGTGCACAATCAACGAGGCCAAAGCGGCTTATTTTGAAGGAG 2472
QY 982 GATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1041
Db 2473 GATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2532
QY 1042 GGCATATTTATTCGCAACGAGTTAGCAGACGAGAGGCTTATGAGCGTGGCCAAAGCA 1101
Db 2533 GGCATATTTATTCGCAACGAGTTAGCAGACGAGAGGCTTATGAGCGTGGCCAAAGCA 2592
QY 1102 GAGTTAAGCAGATGTTACGCCCCCTCTGCAAGCTCTTTCTATTAATCAAGATTTGGTTCAAC 1161
Db 2593 GAGTTAAGCAGATGTTACGCCCCCTCTGCAAGCTCTTTCTATTAATCAAGATTTGGTTATC 2652
QY 1162 TTTGGAGGAGGAGCTGCGCTGAGAGGCCATATCTGAAGAGGATGATGATGATGATGATG 1221
Db 2653 TTTGGAGGAGGAGCTGCGCTGAGAGGCCATATCTGAAGAGGATGATGATGATGATGATG 2712
QY 1222 TGCTATTTGCTAACCGAGACGATCAAGCCCGATATGCTATTTGAGCTGACGCAAGTA 1281
Db 2713 TGTTGTTTGTAGCCAGAACGAGATCAAGCCCGATATGCTATTTGAGCTGACGCAAGTA 2772
QY 1282 TGGAGATTAATTTGATTAACGATATGCTGACGAGTTTCTAATCATGCGGCTGACAGG 1341
Db 2773 TGGAGATTAATTTGATTAACGATATGCTGACGAGTTTCTAATCATGCGGCTGACAGG 2832
QY 1342 AACGAAATTCCTTTGGTGGGCGGAGAGCTGCGAAGCGTTTGAAGAGCAACCATTTTC 1401
Db 2833 AACGAAATTCCTTTGGTGGGCGGAGAGCTGCGAAGCGTTTGAAGAGCAACCATTTTC 2892
QY 1402 GAATGTGATGATTTGACCAAGTTTGG 1427
Db 2893 GAATGTGATGATTTGACCAAGTTTGG 2918
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RESULT 8
US-08-413-135-1

Sequence 1, Application US/08413135
Patent No. 5689042
GENERAL INFORMATION:
APPLICANT: Amasino, Richard M
APPLICANT: Gan, Shuhang
TITLE OF INVENTION: Transgenic Plants with Altered
TITLE OF INVENTION: Senescence Characteristics
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703

COMPUTER READABLE FORM:

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;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/413,135
;; FILING DATE:
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seay, Nicholas J
;; REGISTRATION NUMBER: 27,386
;; REFERENCE/DOCKET NUMBER: 960296, 92808
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 608-251-5000
;; TELEFAX: 608-251-9166
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3183 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "SAG12-1 Promoter DNA"
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US-08-413-135-1
Query Match 28.5%; Score 546.6; DB 2; Length 3183;
Best Local Similarity 82.4%; Pred. No. 7.9e-153;
Matches 627; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

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QY 667 GTATTCAACATATGCAAGACCGATGGATCTACGCTTAATTTTCGCTCAACTTGACAG 726
Db 2159 GTCAATTAATCTTCTTAACCACTGACCTGCACTAATTTTCGCTCAACTTGACAG 2218
QY 727 GAAAGACATGACATGCGATAGCTTTTCCAGACAGACTGCGCTCCAGTCTCTGCTCG 786
Db 2219 GAAAGACATGACATGCGATAGCTTTTCCAGACAGACTGCGCTCCAGTCTCTGCTCG 2278
QY 787 ATGCGCTTCAATGCTGCTCTCAACTATCAACCGGAGCGGAGCAAGTGGAAAGAC 846
Db 2279 ATGCGCTTCAATGCTGCTCTCAACTATCAACCGGAGCGGAGCAAGTGGAAAGAC 2338
QY 847 TGAAGAGACGACTGCTGCTGATCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
Db 2339 TGAAGAGACGACTGCTGCTGATCTTATGATGCTGCTGCTGCTGCTGCTGCTGCTG 2398
QY 907 CCAAGCAAGCTCATGAACGGCTCATTTGCGAGGTGCACAATCAGAGGCCAAAGCGGCGC 966
Db 2399 CCAAGCAAGCTCATGAACGGCTCATTTGCGAGGTGCACAATCAGAGGCCAAAGCGGCGC 2458
QY 967 TTATTTCTGAGGAGGATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1026
Db 2459 TTATTTCTGAGGAGGATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2518
QY 1027 ACGGGATTTTCTGTTGGCATTTATTTGCAACGAGTTAGCAGAGGAGGAGGCTTATGA 1086
Db 2519 GTGCAAGATTTTCTGTTGGCATTTATTTGCAACGAGTTAGCAGAGGAGGAGGCTTATGA 2578
QY 1087 GCGTGGCCAGAACGAGTTAAGCAGATGTTACGCCCCCTCTGACAGGTTCTTTCTATTAATCC 1146
Db 2579 AAGGGCCAGAACGAGTTAAGCAGATGTTACGCCCCCTCTGACAGGTTCTTTCTATTAATCC 2638
QY 1147 AAGAGTTGTTCAACTTTGAGGAGGAGCTGCGCTGAGAGGCCATATCTGAAGAGATCGATG 1206
Db 2639 AAGAGTTGTTCAACTTTGAGGAGGAGCTGCGCTGAGAGGCCATATCTGAAGAGATCGATG 2668
QY 1207 GATATGATATGCGCTGCTATTTGCTACCCAGAACAGATCAAGCCGATATGCTATTTGC 1266
Db 2699 GATATGATATGCGCTGCTATTTGCTACCCAGAACAGATCAAGCCGATATGCTATTTGC 2758
QY 1267 AGCTGACGCGAGATATGAGAAATTAATGATTCAAGGATGCTCAGAGGTTTCTAATCC 1326
Db 2759 AGCTGACGCGAAATATGAGAAATTAATGATTCAAGGATGCTCAGAGGTTTCTAATCC 2818
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QY 1327 ATCCGCTGACAGAAAGAAATTCCTTTGGTGGCGGACAGCTGTGCAAGCTTTG 1386
DB 2819 ATCCGCGCCACAGAAAGAAATTCCTTTGGTGGCGGACAGCTGTGCAAGCTTTG 2878
QY 1387 AAGACCAACATTTGCAATGTGATGATGACCACTTTTG 1427
DB 2879 AAGGTATCTCTTGGAAATGTATGATTAAGCCAGCCCTG 2919

RESULT 9
US-09-434-837-12
; Sequence 12, Application US/09434837
; Patent No. 6759574
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.,
; TITLE OF INVENTION: Plants Having Enhanced Gail Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/09/434,837
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 60/107,185
; EARLIER FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-434-837-12

Query Match 28.4%; Score 545.4; DB 3; Length 723;
Best Local Similarity 84.6%; Pred. No. 7.9e-153;
Matches 612; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 690 ATGATCTACGCTTAATTTTGGTCCAACTTGCACAGGAAACATTCAGCTGCGATAGCT 749
DB 1 ATGACCTGCACTTAATTTTGGTCCAACTTGCACAGGAAACATTCAGCTGCGATAGCT 60
QY 750 CTGCGCCAGCAGATGCGCTCCCACTCTCTGCTGATCGCGTCAATGCTGCTCAA 809
DB 61 CTGCGCCAGCAGACAGGGCTTCCAGTCTTGTGATCGGGTCCAAATGCTGCTCAA 120
QY 810 CTATTAACCGGAAGGGGCGACCAAGTGGAAAGAACTGAAAGCACTGCTCTGAC 869
DB 121 CTATTAACCGGAAGGGGCGACCAAGTGGAAAGAACTGAAAGCACTGCTCTGAC 180
QY 870 CTGATGATCGCCCTTTGGTAAAGGATATCATTAAGCCAGCAAGCTGAACGGCTC 929
DB 181 CTGATGATCGCCCTTTGGTAAAGGATATCATTAAGCCAGCAAGCTGAACGGCTC 240
QY 930 ATTGCGAGGTGCACATCAAGGCAAGGCGGCTTATTTGAGGAGATCTATC 989
DB 241 ATTGCGAGGTGTATATCATTAAGGCAAGGCGGCTTATTTGAGGAGATCTATC 300
QY 990 TCGTGTCTCAGGTGATGCGCAAGTGTATTTGAAACGCGATTTTGTGGCAAT 1049
DB 301 TCGTGTCTCAGGTGATGCGCAAGTGTATTTGAAACGCGATTTTGTGGCAAT 360
QY 1050 ATTGCGAGGTGTGACAGAGAGAGAGCTTCAAGACGCTGCGCAACAGCAATTAAG 1109
DB 361 ATTGCGAGGTGTGACAGAGAGAGAGCTTCAAGACGCTGCGCAACAGCAATTAAG 420
QY 1110 CAGATGTATACGCTCTGCAAGTCTTTCTATTTATCAAGAGTTGTTCAATTTGAGG 1169
DB 421 CAGATGTATACGCTCTGCAAGTCTTTCTATTTATCAAGAGTTGTTCAATTTGAGG 480
QY 1170 GAGCTCGGCTGAGGCGCAATCTGGAAGGATCGATGATATCGATATGCTGCTAT 1229
DB 481 GAGCTCGGCTGAGGCGCAATCTGGAAGGATCGATGATATCGATATGCTGCTAT 540
QY 1230 GCTACCCGAGAACAGATCAAGCGCGGATATGATTTGAGCTGACGAGATATGAGAA 1289

DB 541 GCTACCGAAGACCAATATCAAGCAGATATGCTTATTCAGCTTGCAGCAATATGAGAT 600
QY 1290 AAATTGATTCAGGATATGCTTCAAGATTTTCAATTCATGCGCTGACAGGAACAGAA 1349
DB 601 AAGTGTATTAATGAGATGCTCAGAGATATTTTATTCATTCATGCGCGCAACAGGAACAGAA 660
QY 1350 TTCCCTTTGGTGGGCGCAGCTGTGGAAGGTTTGAAGAACCACTTTGGAATGTGA 1409
DB 661 TTCCCTTTGGTGGGCGCAGCTGTGGAAGGTTTGAAGAACCACTTTGGAATGTGA 720
QY 1410 TAG 1412
DB 721 TAG 723

RESULT 10
US-09-434-837-5
; Sequence 5, Application US/09434837
; Patent No. 6759574
; GENERAL INFORMATION:
; APPLICANT: Ream, Walt et al.,
; TITLE OF INVENTION: Plants Having Enhanced Gail Resistance and
; TITLE OF INVENTION: Methods and Compositions for Producing the Same
; FILE REFERENCE: 53629
; CURRENT APPLICATION NUMBER: US/09/434,837
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 60/107,185
; EARLIER FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-434-837-5

Query Match 28.1%; Score 539.4; DB 3; Length 747;
Best Local Similarity 84.5%; Pred. No. 5.1e-151;
Matches 606; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 696 CTAGCTTAATTTTGGTCCAACTTGCACAGGAAAGACATGAGCTGCGATAGCTTCTGCC 755
DB 18 CTGATCTTAATTTTGGTCCAACTTGCACAGGAAAGACATGAGCTGCGATAGCTTCTGCC 77
QY 756 CAGCAGATGCGCTCCCACTCTCTGCTGATCGCGTCAATGCTGCTCAACTATCA 815
DB 78 CAGCAGATGCGCTCCCACTCTCTGCTGATCGCGTCAATGCTGCTCAACTATCA 137
QY 816 ACCGGAAGCGGCGCAACAGTGAAGAACTGAAAGGACGATCGTCTGACTTGAT 875
DB 138 ACCGGAAGCGGCGCAACAGTGAAGAACTGAAAGGACGATCGTCTGACTTGAT 197
QY 876 GATGCGCTTTGGTAAAGGATATCATTAAGCCAGCAAGCTGAACGGCTCAATTGCG 935
DB 198 GATGCGCTTTGGTAAAGGATATCATTAAGCCAGCAAGCTGAACGGCTCAATTGCG 257
QY 936 GAGGTGCAATCAAGAGCGGCGCTTATTTGAGGAGATCTATCTGTTG 995
DB 258 GAGGTGATATATCAAGAGCGGCGCTTATTTGAGGAGATCTATCTGTTG 317
QY 996 CTCAGGTGATGCGGCAAGTGTATTTGAAACGCGATTTTGTGGCAATTAATTCGC 1055
DB 318 CTCAGGTGATGCGGCAAGTGTATTTGAAACGCGATTTTGTGGCAATTAATTCGC 377
QY 1056 AAGAGTTAGAGAGAGAGAGCTTATGAGCGTGGCAAGACAGATTAACAGATG 1115
DB 378 CACAAGTTAGAGAGAGAGAGCTTATGAGCGTGGCAAGACAGATTAACAGATG 437
QY 1116 TTACGCGCTCTGAGGCTTTTCTATTTATCAAGATTTGTTCACTTTGAGGAGAGCT 1175
DB 438 TTGACCCCGCTGAGGCGCAATTTATTTATCAAGATTTGTTTATTTGGAATGAAGCT 497
QY 1176 CCGCTGAGGCGCAATCTGGAAGGATGATGATATGCTTCTGCTATTTGCTAAC 1235

[illegible]

| Query Match | 12.0% | Score 231.2 | DB 2 | Length 584 |
|-----------------------|----------------|--|------------|------------|
| Best Local Similarity | 70.6% | Pred No. 1.1e-58 | | |
| Matches 479 | Conservative 0 | Mismatches 78 | Indels 121 | Gaps 8 |
| Db | 690 | ATGATCTACGCTCTAATTTTCGGTCCAACTTGACAGGAAGAACATCGACTCGATAGCT | 749 | |
| Qy | 1 | ATGAGCTGATCTTAATTTTCGGTCAAACTTGACAGGAAGAACAGCAGCCGATAGCT | 60 | |
| Db | 750 | CTTGCCCGACGACGCTGCTCCCACTCTCTCGCTCGATCGGCTCCAAAGCTGCTCTCA | 809 | |
| Qy | 61 | CTTGCCCGACGACGAGGCT-----GGGTCCAAAGCTGCTCTCA | 100 | |
| Db | 810 | CTATCAACCGGAAGCGGCGACCAACAGTGAAGAACTGAAGAAAGCAAGCTGCTGTAC | 869 | |
| Qy | 101 | CTATCAACCGGAAGCGGCGACCAACAGTGAAGAACTGAAGAAAGCAAGCTGCTGTAC | 160 | |
| Db | 870 | CTTGATGATCGCCCTTTGGTAAAGGATCATTAACGCCAAGCAAGCTATGACGGCTC | 929 | |
| Qy | 161 | -----GGAGGGTATCATCGACGCCAACCAAGCTCATATAGGCTG | 200 | |
| Db | 930 | ATTGCGGAGTGCACAATCAGAGGCCAAAGCGGGCTATTCTTGAGGAGAGATCTATC | 989 | |
| Qy | 201 | ATCGAGGAGGTATTAATCATAGGCCCAACGGCGGGCTTA----- | 240 | |

| | | | |
|----|------|---|-------|
| OY | 990 | TGCTGTCCAGGTGCATGGCGCAAACTGGTATTGGAAACGGGATTTTCGTGGCATATT | 10439 |
| Dd | 241 | TGTTTGCTCCTAAGTATGATGAGCGGAAGAAGCTATTATGGATGCGAGATTTTCGTTGGCATATT | 300 |
| OY | 1050 | ATTGCCAACGAGTTAGCACAGCAGGAGAGACTTCATGACGCTGGGCCAACAACAGAGTTTAAG | 1109 |
| Dd | 301 | ATTGCCAACAGTTATCCCGAC-----GGCCAAAGCCAGATTTAG | 340 |
| OY | 1110 | -CAGATGTTAGCCCCCTCTGCAAGTCTTTCTATTATTCCAAAGATTGTTCAACTTTGGAG | 1168 |
| Dd | 341 | CCAGATGTTGCAACCCCCCTGCAGAGGCATTCTATTATTC-AGAGTTGGTTTTATCTTTGGAA | 399 |
| OY | 1169 | GGAAGCTCGGCTGAGAGCCCATACTGGAGAGGATGCATGGATATTCGATATGCCCTGCTATT | 1228 |
| Dd | 400 | T-----TTCTGAAAAGAAATCGATGATATCGATATGCCATTGGTT | 440 |
| OY | 1229 | TGCTACCAGAACCGATCATCGCCCGATATGCTATTATGAGCTCGACGCGATATGAGAA | 1288 |
| Dd | 441 | TGCTAGCCAGAACCGATCATCGGCGAGATATGCTATTGAG----- | 480 |
| OY | 1289 | TAAATGTAATTCACGGTATCGCTCAGAGATTTCTAATCCATCGCGCTGCACAGAACGAA | 1348 |
| Dd | 481 | TAAAGTGAATTAATGGATCGCTCATGAGATATTTCATCCATCGCGCCCAACGAGGACAGAA | 540 |
| OY | 1349 | ATTCCCTTTGGTGGGCGC | 1366 |
| Dd | 541 | ATTCCCCCAAGTTAAAGC | 558 |

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RESULT 13
US-09-621-976-2813
? Sequence 2813, Application US/09621976
? Patent No. 6639063
? GENERAL INFORMATION:
? APPLICANT: Dumas Milne Edwards, J.B.
? APPLICANT: Jobert, S.
? TITLE OF INVENTION: ESTS and Encoded Human Proteins.
? FILE REFERENCE: GENSET.054PR2
? CURRENT APPLICATION NUMBER: US/09/621.976
? NUMBER OF SEQ ID NOS: 19335
? SOFTWARE: Patent.pm
? SEQ ID NO 2813
? LENGTH: 832
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 235..339
US-09-621-976-2813

Query Match      2.3% Score 44.8; DB 3; Length 832;
Best Local Similarity 12.3%; Pred. No. 0.0097;
Matches 37; Conservative 138; Mismatches 145; Indels 0; Gaps 0;

QY    1423 TTTTGTTCAGACTTGCGCTATTGTAATAAGATGGTTCGTTCTTTGTGTGTGGTGCTG 1482
Db     : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
        WTKKMSWSMYMKWYIMKTITVWMRRKKKAMKWKMTWTWYMRAMNGTYKKAMCR 75

QY    1483 TGTGATAGAGCAAGTGGTTGAACCTGTTTTACTGCGTTATTTCAGCTCTTGAC 1542
Db     |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
        TKTKKKKKKKGGMMWMCWRSSYMAWMTFTVTGYAYRSWWMYRRCWKKRAYRTTCC 135

QY    1543 GATGTTTACAAATATATATATATTTGAAAATTTGCGTTTATATTCGTAGAAGAAATAA 1602
Db     |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
        YSSKGMTWKKRWKKAMLTWMMKXTIYYNAATRYMWMCMCKWRBASMWYCWMMWGAKRMST 135

QY    1603 TGCTPAGATAGCCGCTATCAAATTTTAGCAAAAAATTTGTAAGAGTCTTTTATGCGGTG 1662
Db     ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
        WRKRSYSVASASARCCYSCSGWAMSWYIMRMWRMGWATGACGMKWRASCWRRRYAG 255

QY    1663 AGGTTGTGCATTTTTCATCATGTGTGCGTAAAGAGATTACGATATCATACTGTAATAAA 1722

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[illegible]

| | | | | |
|---|-------|--|----------------|------------|
| Query Match | 2.2% | Score 43 | DB 3 | Length 832 |
| Best Local Similarity | 10.2% | Pred. No. 0.033 | | |
| Matches | 37 | Conservative 167 | Mismatches 157 | Indels 0 |
| | | | Gaps | 0 |
| Oy | 6 | CCGTTACAGATTGACAGCTTTTGTAAATTCATATTATGCAATCTGGATGTTAAATA | 65 | |
| Db | 362 | YYMTWMKTMWYTTTYTWRMMMKKARRWYWMSTYACASRYKTYTMGWMWMMKRM | 303 | |
| Oy | 66 | CGAATGTAATGCCGTAGAAATATGTAATTTATGTAATTATCTTCACTAGTTGAAGTT | 125 | |
| Db | 302 | STRWCVWCMCKCVRGRCAWMTMARBMWSYAMGKKMSRMSAMSCMTMYKKGSTYW | 243 | |
| Oy | 126 | TGCATATATAGCTAATCTAAATTAATAAAATATAGTCTGCCGCAATTTGTTCAATGCG | 185 | |
| Db | 242 | TMKTCATWCKWYKWRMMSKTCWSSRGWTSYSTSBSYSWYMSMWTMCWMMWR | 183 | |
| Oy | 186 | GCCGTTATTTAAAAATATCTTTGATTTTGTACAGACAGACGCTCAGAGAGTAAT | 245 | |
| Db | 182 | WMSYTWYAMCKKWRRIATYTRRLAMWMAAVTMMYMMWMAWMSRRGAATRTMMWG | 123 | |
| Oy | 246 | AAAAAGCGCTGTTGTAAATATGCTATCATATGTGCCGCTATAGGCCATTTAAGT | 305 | |
| Db | 122 | YRWYMRKKSYSRTHCANAYAMKTRBSYWCWRMKWR CMMWMMWMAAYGKTMWBAWMT | 63 | |
| Oy | 306 | TCAATTGTGAATATGCCGCCCTTATTTTGACGCTCATCAATATCAATATTTAAATAAT | 365 | |
| Db | 62 | RYWYMWAMWMMRWMTMMYMMYWRMKRMMWRKWRSMWMMWMAWMTWAAAMWWR | 3 | |
| Oy | 366 | C 366 | | |
| Db | 2 | Y 2 | | |
| RESULT 15 | | | | |
| US-09-806-708B-22/c | | | | |
| Sequence 22, Application US/09806708B | | | | |
| Patent No. 678342 | | | | |
| GENERAL INFORMATION: | | | | |
| APPLICANT: The University of British Columbia | | | | |
| TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants | | | | |
| FILE REFERENCE: 4810-58741 | | | | |
| CURRENT APPLICATION NUMBER: US/09/806,708B | | | | |
| CURRENT FILING DATE: 2001-04-03 | | | | |
| PRIOR APPLICATION NUMBER: US 60/147,133 | | | | |
| PRIOR FILING DATE: 1999-08-04 | | | | |
| NUMBER OF SEQ. ID NOS: 23 | | | | |

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; SOFTWARE: Patentin version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.C., L.a., and B.n. FAEl promoters
US-09-806-708B-22
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Query Match 2.2%; Score 42.4; DB 3; Length 1141;

Best Local Similarity 12.1%; Pred. No. 0.06; Mismatches 274; Indels 9; Gaps 3;

```
Matches 73; Conservative 246; Mismatches 274; Indels 9; Gaps 3;

QY 12 CAAGTATGCGCGTTTGTAATGATGATTAATGATGATGATGTT--TAATAAGCAA 69
DB 705 YAAATNNWGCWNNNTDARTNNTTVMRRMNTTKTRWYSTTRRHHTGATNNNNNNNN 646
QY 70 TGTATGCGCGTAGAATAATGATTTTATGATTTATCTTCACTANGTTGAAGTTGCA 129
DB 645 NNNNNNSCCTCTRMMTBMTMGDMTRKVKWRDPTCTYDVWADSVWVWYANWWR 586
QY 130 ATAATATGCTATGTAATAATTAATAATATGATGCTGCGCATTTGTTCAATGCGCG 189
DB 585 RDVYTRNNITCKSYAHSYWSNNAMWRRYSARNSSMARWTRNNWMSGVRRWA 526
QY 190 TTATTTCAAAATCTTTGATTTGTTTACGAGCAGACGATCGAGAGTAATAATAA 249
DB 525 GTMWRHRNNNTDRTYRWMKWRABITTYDSGNKSKSMRGNNWRAMQWMAANNDA 466
QY 250 GACGCTGTT--GTTAGAAATGCTATCATATGTCGCCAGCTATAGGCGCATTTAAGTT 306
DB 465 GAMDHTYMGNTWMMWRAMWMMWMCRRAYCCNNNNNRACVHKKKMRWTKYWMX 406
QY 307 CAATTGTAATAGCGCCCTTATTTGACGCTCATCAATCAATTAATAATAATC 366
DB 405 AACNNNNBRAMYMRVAMWMSRDNTTDM--WMTSDWBHMYTVDYTWRRANNNNN 350
QY 367 TCACCTGTGCGCAGCATGATGTAATACGACAGAAAGTAGAGTAATCGCGAAAA 426
DB 349 NNMRBCKTTSMMWMDHNHTCTYGNNTGSAVBMAASMAAGASNEVTYNWCMRTYM 290
QY 427 ACGTCGCCAGTGCATAGCGCGCTCCGATTTGCTGATTTAGCTTAATTGA 486
DB 289 GKTMTNNNNNNKAWYRTKTVAMCNRYYUDAVTWBKRNYCYAYBMYBMYGKH 230
QY 487 CTTAAGGCGCTGCTAGTACAAATGCTTCAAGAGACAGCCATGCCCACTT 546
DB 229 BWRRAABHRSMWVVKCRNKYVSWHYHAMRYBKABAVGCGNNWKMMAHHHCATNN 170
QY 547 TGTGAAACAGAGTTCCTTTTGGAAGAACCTAAGCACTTCTTCAAGAGGAA 606
DB 169 NMMWMMYAYHHMKGAATNNKTAABDDHBAHVXYTWYRWYWCAMCMNAKAKVR 110
QY 607 TA 608
DB 109 TA 108
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Search completed: June 26, 2006, 18:55:59
Job time : 344 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2006, 18:36:54 ; Search time 8253 Seconds

(without alignments)
13002.447 Million cell updates/sec

Title: US-10-817-483-1

Perfect score: 1919

Sequence: 1 ggatccgcgtacaaagtctg.....tacgcattatagacaagctt 1919

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 48236798 segs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : EST:*

1: gb_est1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB ID | Description |
|------------|-------|---------|--------------|-------|-------------|
| 1 | 55.2 | 2.9 | 1099 | 14 | CNS06PYL |
| 2 | 54.2 | 2.8 | 1101 | 14 | CNS016TA |
| 3 | 52 | 2.7 | 754 | 11 | BH483858 |
| 4 | 52 | 2.7 | 786 | 11 | BH445413 |
| 5 | 52 | 2.7 | 796 | 11 | BH514721 |
| 6 | 51 | 2.7 | 1380 | 12 | CC190214 |
| 7 | 51 | 2.7 | 1489 | 14 | AG350139 |
| 8 | 50.8 | 2.6 | 859 | 14 | CNS00KTL |
| 9 | 50.6 | 2.6 | 742 | 11 | BZ390485 |
| 10 | 50.6 | 2.6 | 1101 | 14 | CNS01JUM |
| 11 | 49.4 | 2.6 | 813 | 3 | BME57710 |
| 12 | 49.4 | 2.6 | 878 | 14 | CNS0187R |
| 13 | 49.2 | 2.6 | 1250 | 12 | CL048827 |
| 14 | 49 | 2.6 | 292 | 2 | B1742580 |
| 15 | 49 | 2.6 | 1203 | 14 | CNS015WU |
| 16 | 48.8 | 2.5 | 1300 | 7 | BE420576 |
| 17 | 48.6 | 2.5 | 876 | 13 | CZ529924 |
| 18 | 48.6 | 2.5 | 1078 | 12 | CU031456 |
| 19 | 48.6 | 2.5 | 1201 | 14 | CNS016ET |

| | | | | | |
|----|------|-----|------|----|----------|
| 20 | 48.4 | 2.5 | 1097 | 12 | CU024868 |
| 21 | 48.2 | 2.5 | 881 | 11 | AZ681832 |
| 22 | 48.2 | 2.5 | 1084 | 14 | CNS0025S |
| 23 | 48 | 2.5 | 1201 | 14 | CNS016DB |
| 24 | 47.8 | 2.5 | 322 | 14 | DE042918 |
| 25 | 47.8 | 2.5 | 938 | 14 | CNS006TY |
| 26 | 47.4 | 2.5 | 867 | 14 | CNS00CX5 |
| 27 | 47.4 | 2.5 | 1371 | 9 | DN662120 |
| 28 | 47.2 | 2.5 | 500 | 1 | AU087545 |
| 29 | 47.2 | 2.5 | 500 | 3 | BP114521 |
| 30 | 47.2 | 2.5 | 639 | 13 | CW330724 |
| 31 | 47.2 | 2.5 | 732 | 13 | CM439569 |
| 32 | 47.2 | 2.5 | 942 | 3 | BP930773 |
| 33 | 47 | 2.4 | 389 | 9 | DN197640 |
| 34 | 47 | 2.4 | 819 | 13 | CZ536319 |
| 35 | 47 | 2.4 | 1184 | 14 | CNS04P4P |
| 36 | 46.8 | 2.4 | 546 | 3 | BM620921 |
| 37 | 46.8 | 2.4 | 665 | 3 | BM634198 |
| 38 | 46.8 | 2.4 | 826 | 13 | DU068950 |
| 39 | 46.8 | 2.4 | 839 | 13 | CZ536111 |
| 40 | 46.8 | 2.4 | 1225 | 14 | CNS0161D |
| 41 | 46.6 | 2.4 | 695 | 3 | BP513401 |
| 42 | 46.6 | 2.4 | 750 | 14 | CNS011ID |
| 43 | 46.6 | 2.4 | 796 | 14 | CNS0118D |
| 44 | 46.6 | 2.4 | 865 | 11 | AZ693005 |
| 45 | 46.6 | 2.4 | 866 | 11 | AZ672468 |

ALIGNMENTS

| | | | | | |
|------------|---|------------------------|-----|--------|-----------------|
| RESULT 1 | CNS06PYL | 1099 bp | DNA | linear | GSS 05-JUL-2001 |
| LOCUS | T7 end of clone AW0A001B06 of library AW0A | from strain CLUB 89 of | | | |
| DEFINITION | Yarrowia lipolytica, genomic survey sequence. | | | | |
| ACCESSION | AL009987 | GI:12177872 | | | |
| VERSION | AL009987.1 | | | | |
| KEYWORDS | GSS. | | | | |
| SOURCE | Yarrowia lipolytica | | | | |
| ORGANISM | Yarrowia lipolytica | | | | |
| REFERENCE | Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; | | | | |
| AUTHORS | Souci t,J.L., Aigle,M., Artiguenave,F., Blandin,G., | | | | |
| | 1 (bases 1 to 1099) | | | | |
| | de Montigny,J., Dujon,B., Duren,P., Lepingle,A., Llorente,B., | | | | |
| | Malpertuy,A., Neuviglise,C., Ozier-Kalogeropoulos,O., Potier,S., | | | | |
| | Saurin,W., Tekala,F., Toffano-Nic che,C., Wesolowski-Louvel,M., | | | | |
| | Winker,P. and Weissenbach,J. | | | | |
| TITLE | Genomic exploration of the hemiascomycetous yeasts: 1. A set of | | | | |
| | Yeast species for molecular evolution studies | | | | |
| JOURNAL | FEBS Lett. 487 (1), 95-100 (2000) | | | | |
| PUBMED | 11152876 | | | | |
| REFERENCE | 2 (bases 1 to 1099) | | | | |
| AUTHORS | Casaregola,S., Neuviglise,C., Lepingle,A., Bon,E., Feyn rol,C., | | | | |
| | Artiguenave,F., Winker,P. and Galliardin,C. | | | | |
| TITLE | Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia | | | | |
| | lipolytica | | | | |
| JOURNAL | FEBS Lett. 487 (1), 95-100 (2000) | | | | |
| PUBMED | 11152892 | | | | |
| REFERENCE | 3 (bases 1 to 1099) | | | | |
| AUTHORS | Genoscope. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (07-SEP-2000) Genoscope - Centre National de S quenc age, | | | | |
| | 2 rue Gaston Cr mieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : | | | | |
| | seque genoscope.cns.fr - Web : www.genoscope.cns.fr) | | | | |
| COMMENT | This GSS is part of a random genomic sequencing program of thirteen | | | | |
| | yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces | | | | |
| | exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, | | | | |
| | Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces | | | | |
| | lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia | | | | |
| | angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, | | | | |

Query Match 2.7%; Score 52; DB 11; Length 796;
 Best Local Similarity 53.4%; Pred. No. 0.044;
 Matches 109; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

79 GTAGAAATGATATTTATTTATTTATTTCTTCACTATGTAAGTTGCAATAATGC 138
 280 GCATACCAATGTTTTTTTATTTATTAATAAATCTTAATTAACATGATTGAAATATTA 339
 139 TAATGTAATAATTAATAAATTAATGATCGCCGCAATTTGTTCAATGGCCGTTATTTCAA 198
 340 TACTACGTAATTAATAAAGTATTAATGACCTATTAATTAATAAATTTTATTTAGTA 399
 199 AAATATCTTATTTTGTAGAGACACACATCGCAGAGTAATAAGACGCTT 258
 400 AGAATATTTTGAATTTTCTTCACACAGATTTTGCAATAAATAAATAAACAAGT 459

259 GTTAAGAAATGTCATCATATGTG 282
 460 TTATAGATGAATTTTATATGTG 483

Db

RESULT 6
 LOCUS CCI90214 1380 bp DNA linear GSS 08-MAY-2003
 DEFINITION CH261-3712_RM1.1 CH261 Gallus gallus genomic clone CH261-3712,
 genomic survey sequence.
 ACCESSION CCI90214
 VERSION CCI90214.1 GI:30435240
 KEYWORDS GSS.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianine; Gallus.
 1 (bases 1 to 1380)
 Kremiczki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
 Warren, W., Graves, T., Mardis, E. and Wilson, R.
 Gallus gallus BAC End Reads
 Unpublished (2003)
 Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@wustl.wustl.edu
 Insert Length: 182000 Std Error: 0.00
 Seq primer: RM1 TACGACTCATATAGGGAGA
 Class: BAC ends
 High quality sequence start: 266
 High quality sequence stop: 809.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-3712"
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 /note="Vector: pFARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CH261 Female Chicken library - For library and clone
 ordering information: http://www.chori.org/bacpac"

ORIGIN

Query Match 2.7%; Score 51; DB 12; Length 1380;
 Best Local Similarity 47.3%; Pred. No. 0.089;
 Matches 167; Conservative 0; Mismatches 185; Indels 1; Gaps 1;

16 TATTCACGCTTTGTAATGCAATTAATGCAATCTGATGTTAATACAAATGTAAT 75
 1006 TAGTCAAAATTTTAAATTTTAAATGTTTAAATGTTTAAATTTTAAATTTGCTT 1065
 76 GGCGTAGAAATATGATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTT 134

Db

Db

1066 TTTTAAATTAATAAATAATTAATTTCTTAAAAAAGTAATTTGTTAAACA 1125
 135 ATGCTATATGTAATTAATAAATTAATGATCTGCCGCAATTTGTTCAATGGCCGTTATT 194
 1126 AAAAAAATTTCTTTAAAAATTTTAAAAATTAATTTGTTAAAAAGTTGGTTAAA 1185
 195 TCAAAATATCTTTGATTTTGTATGTCAGAGCAACGACTGACGAGAAATTAATAAGACGC 254
 1186 TCAAAACACTTTATTTTAAAAAGGGTATTAATTTCCCTTAATTTTAAAAAANGT 1245
 255 TGTGTTAGAAATTTGTCATCATATGTCGCCAGCTATAGGCCCATTTAAGTCAATGTG 314
 1246 TTTTGTAATAATTTCAATTAATTAATTTCCNCTTTTTCACCATGANAATTAATTAATTTG 1305

315 AAATAGCCGCCCTTATTTGACGCTCATGAAATCAATTAATAAATATCT 367
 1306 GAAAAAATTTTCAATTTGTTTTCAGNCANATTAATTAATTAATTTTCT 1358

Db

RESULT 7
 LOCUS AG350139 1489 bp DNA linear GSS 18-DEC-2004
 DEFINITION Mus musculus molossinus DNA, clone:MSWg01-146K14.TJ, genomic survey
 sequence.
 ACCESSION AG350139
 VERSION AG350139.1 GI:47923449
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus (Japanese wild mouse)
 ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidae; Muridae; Murine; Mus.
 1
 Abe, K., Noguchi, H., Tagawa, K., Yuzurika, M., Toyoda, A., Kojima, T.,
 Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaki, K. and
 Shiroishi, T.
 Contribution of Asian mouse subspecies Mus musculus molossinus to
 genomic constitution of strain C57BL/6J, as defined by BAC-end
 sequence-SNP analysis
 Genome Res. 14 (12), 2439-2447 (2004)
 15574823
 2 (bases 1 to 1489)
 Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
 Direct Submission
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
 (E-mail: hattori@ipc.riken.jp, URL: http://hgp.igsc.riken.go.jp/,
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 Clones are derived from the mouse BAC library MSWg01. For BAC
 library availability, please contact Kuniya Abe (abe@ipc.riken.jp).
 Tsukuba Institute, Bio Resource Center,
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@ipc.riken.jp
 PRIMERS
 Sequencing : TJ
 LIBRARY : PBACE3.6
 Vector : EcoRI
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.
 Location/Qualifiers
 1..1489
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 /clone="MSWg01-146K14.TJ"
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ORIGIN


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/note="end : TEr3"
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FEATURES
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                /clone="EIND15"
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                /note="Vector: pHOS2; Site 1: BstXI; Total genomic DNA was isolated from early log phase trophozoites of E. invadens"

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QY 139 TAATGTAATAATTAATGATGCGGCGATTTGTCGAATGGCGGTATTTCGA 198
DB 449 TTAATATTTATTTAAATTAATTAATTAATTTTAAAGCTCATCCTTAA 390
QY 199 AATATCTTGTGATTTGTTACGAGCAACGACTCGAGAGTAATTAAGAAGCTGTT 258
DB 389 AATATCTTGTGATTTGTTACGAGCAACGACTCGAGAGTAATTAAGAAGCTGTT 330
QY 259 GTTAAGAAATGTCATCATATGCGCCAGCTATAGGCCATTAAAGTTCAATTGTAAT 318
DB 329 TTAATATCTTGTGATTTGTTACGAGCAACGACTCGAGAGTAATTAAGAAGCTGTT 270
QY 319 AGCGGCGCTTATTTGACGCTCATCAATCAATTAATTAATTAATTCACCTGCGG 378
DB 269 TACATATTTAAATGATTTTCCACATTAATCTTTTAAATTAATTAATTC 210
QY 379 CAGCAATGATGTAATTA 395
DB 209 GAGAAATTAATTAATTA 193
RESULT 12
CNS0187R/c 878 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BAC04E04 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL108993.1 GI:5629297
VERSION 1
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 878)
Genoscope.
COMMENTS Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : segreif@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billard at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.
FEATURES
source Location/Qualifiers
1..878
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN04E04"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : SP6"
ORIGIN
Query Match 2.6%; Score 49.4; DB 14; Length 878;
Best Local Similarity 25.2%; Pred. No. 0.22;
Matches 80; Conservative 93; Mismatches 144; Indels 0; Gaps 0;
QY 1397 ATTTGGAATGATGATGACACCAAGTTTGTTCGACTGCTATTTGAATGAAT 1456
DB 335 WTGTAAATTTKTTTATTTKTTTATTTTATTTTATTTTATTTTATTTTATTTT 276
QY 1457 GTTCGTTCTTTGTGTTGTGTTGTGTTGTGATAGGCAAGTGTGAATCTGTTT 1516
DB 275 TTKMKMKMTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 216
QY 1517 ACTGTTATTTTACGCTCTTTCGACGATGTTTACAAATATTAATTTGTGAATTTG 1576

DB 215 WWWWCTTWWTTTMMWTTTMMWTTTAAATKMMWTTTAAATACMAATVATGAGCCAAAGW 156
QY 1577 GTTTATATTCGTAGAACGAATTAATGTAATAGCCGTTATCAAAATTTAGCAAAA 1636
DB 155 KMTTATTTTMMWTTTMMWTTTMMWTTTMMWTTTMMWTTTMMWTTTMMWTTTMM 96
QY 1637 ATTTGTAAGTTCTTTTATTTGCGGTGAGGTGTGCACTTTTCAATTTGTCGGTAA 1696
DB 95 TWTWTTTMMWTTTMMWTTTMMWTTTMMWTTTMMWTTTMMWTTTMMWTTTMMWTT 36
QY 1697 GTTACGATATTCATTA 1713
DB 35 TTTACGACACCAATTA 19
RESULT 13
CL048827/c 1250 bp DNA linear GSS 31-DEC-2003
LOCUS CH216-68N9_RM1.1 CH216 Xenopus tropicalis genomic clone CH216-68N9,
DEFINITION genomic survey sequence.
ACCESSION CL048827
VERSION CL048827.1 GI:40504740
KEYWORDS GSS.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1250)
Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E., and Wilson, R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
CONTACT: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: RM1 TACGACTCATATAGGAGGA
CLASS: BAC ends
High quality sequence start: 172
High quality sequence stop: 611.
FEATURES
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/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-68N9"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
ORIGIN
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Best Local Similarity 51.9%; Pred. No. 0.26;
Matches 111; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 1400 TCGAATGATGATGATGACACCAAGTTTGTTCGACTGCTATTTGAATGAATGTT 1459
DB 1018 TTGAATTTTAAATTAATTAATGATTTTATTAATTTTAAATTTTAAATTTTAA 959
QY 1460 CGTTCTTTGTGTTGTGTTGTGTTGTGATAGGCAAGTGTGAATCTGTTTACT 1519
DB 958 CTCTTTTAAATATGCTTTTGTGTTGTGTTGAAGGAAATTTTAAATTTTGTGCA 899
QY 1520 GGTATATTTTACGCTCTTTCGACGATGTTTACAAATATTAATTTGTAATTTGTT 1579
DB 898 ATTTTTCGAGTTAAATTTGACCAATTTTATTTTATTTTATTTTATTTTATTTTCC 839

Qy 1580 TTATATTCGTAGAACAAATAATAGTACGTATA 1613
Db 838 ATATATTAATGAAATAGAAAATGGTTATTTTA 805

RESULT 14
BI742580/c
LOCUS BI742580
DEFINITION K552g12.y4 Strongyloides ratti L1 PAMP1 v3 Chiapelli McCarter
ACCESSION BI742580
VERSION BI742580
KEYWORDS EST.
SOURCE Strongyloides ratti
ORGANISM Strongyloides ratti
REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida;
Panagrolaimoidea; Strongyloidea; Strongyloides.
1 (bases 1 to 292)
AUTHORS Thompson, F.J., Mitreva, M., Barker, G.L., Martin, J., Waterson, R.H.,
McCarter, J.P. and Viney, M.E.
COMMENT An expressed sequence tag analysis of the life-cycle of the
parasitic nematode Strongyloides ratti
Mol. Biochem. Parasitol. 142 (1), 32-46 (2005)
15907559
CONTACT: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@waterson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bcm@lapel.watson.wustl.edu & jmcarter@watson.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Seq primer: -40RP from Gibco
High quality sequence stop: 285.
FEATURES
source
Location/Qualifiers
1..292
/organism="Strongyloides ratti"
/mol_type="mRNA"
/db_xref="taxon:34506"
/dev_stage="L1"
/lab_host="DH10B"
/clone_lib="Strongyloides ratti L1 PAMP1 v3 Chiapelli
McCarter"
/note="Vector: PAMP1 (Gibco); The library was constructed
by Brandi Chiapelli and Dr. James McCarter at Washington
University, St. Louis. The cDNA was made by using
Dynabead oligo-dT priming (Dynal). PCR based library
using a modified protocol from the SMART PCR cDNA
Synthesis Kit from Clontech. Directionally cloned into the
UDG sites of PAMP1. Nematodes were provided by Dr. Mark
Viney of Bristol, UK."

ORIGIN
Query Match 2.6%; Score 49; DB 2; Length 292;
Best Local Similarity 55.6%; Pred. No. 0.22;
Matches 94; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
Qy 86 TATGATTTTATGATTTATCTTCACTAGTGAAGTTGCAATAATAGTAAAGTA 145
Db 173 TTTTATTTTATTAATGATATTTATTTATTTAAAGATTAACAATAATGAAATTTAA 114
Qy 146 AAATTTAAAAATTAATGATCGCCGATTTGTTCAATGGCCGTTATTTCAAAAATATC 205
Db 113 CGATTAATAACATTTATATCAAAAACATAAGATTAATAATATATCTTTGTTAAAAATATC 54
Qy 206 TTTGATTTTGTTCAGAGCAACGATGCGAGGAAGTAAATAAAGAGCG 254
Db 53 TTAATTTTATTCGAACCATAGATTAATGTTAAATATATATACATTACAC 5

RESULT 15
CNS015WU
LOCUS CNS015WU 1203 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence Sp6 end of BAC
BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106008
ACCESSION AL106008.1 GI:5619558
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1203)
REFERENCE Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqret@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billard at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.
FEATURES
source
Location/Qualifiers
1..1203
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN15E10"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : Sp6"

ORIGIN
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Best Local Similarity 35.4%; Pred. No. 0.29;
Matches 86; Conservative 48; Mismatches 109; Indels 0; Gaps 0;
Qy 1444 ATTGAATAGAGCTTCGTTCTTGTGCTGCTGCTGTGTGATAGGCAAGTGGTT 1503
Db 953 ATTWTATTAAT 1012
Qy 1504 GAAACTGTTTTCAGTTTATTTTCAGTCTCTTGACGATGTTTACAAATATATAT 1563
Db 1013 ATATTTTAT 1072
Qy 1564 TGTGAAATATGCTTTTATATGTAAGAACGAATTAATAGTAAGTAAAGCGTTATCA 1623
Db 1073 TWTWAAABAATATTTTWTWTTTATTAAMWAMWATATTAAMWATATATATAT 1132
Qy 1624 AAATTTAGCAAAATTTGTTAAAGTCTTTTATGCGGTGAGTGTGACCTTTCATCAT 1683
Db 1133 WATWTTAT 1192
Qy 1684 TGT 1686
Db 1193 TAT 1195

Search completed: June 26, 2006, 23:50:15
Job time : 8258 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2006, 19:20:37 ; Search time 2432 Seconds
(without alignments)
9695.712 Million cell updates/sec

Title: US-10-817-483-1

Perfect score: 1919

Sequence: 1 ggatccgcgtacacagctg.....taagcattacagacagctt 1919

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA Main:*

1: /EMC_Celerra_SIDS3/prodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/prodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/prodata/2/pubpna/US09_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|---------------------|
| 1 | 1919 | 100.0 | 1919 | 9 | US-10-817-483-1 |
| 2 | 1089.8 | 56.8 | 1997 | 8 | US-10-465-008-1 |
| 3 | 956.8 | 49.9 | 1988 | 8 | US-10-365-723-2 |
| 4 | 722 | 37.6 | 3017 | 13 | US-11-139-461-12 |
| 5 | 720.4 | 37.5 | 2722 | 13 | US-11-139-461-8 |
| 6 | 720.4 | 37.5 | 2722 | 13 | US-11-139-461-9 |
| 7 | 720.4 | 37.5 | 5622 | 13 | US-11-139-461-7 |
| 8 | 720 | 37.5 | 723 | 7 | US-10-409-701-2 |
| 9 | 717 | 37.4 | 717 | 7 | US-10-369-493-38935 |
| 10 | 583.8 | 30.4 | 723 | 9 | US-10-821-711-2 |
| 11 | 583.6 | 30.4 | 720 | 7 | US-10-369-493-35042 |
| 12 | 583.6 | 30.4 | 720 | 7 | US-10-369-493-38138 |
| 13 | 583.6 | 30.4 | 720 | 7 | US-10-369-493-38138 |
| 14 | 582.2 | 30.3 | 723 | 16 | US-11-156-084-1 |
| 15 | 582.2 | 30.3 | 723 | 16 | US-11-156-084-1 |
| 16 | 582 | 30.3 | 720 | 7 | US-10-369-493-38954 |
| 17 | 582 | 30.3 | 720 | 7 | US-10-369-493-38969 |

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|----|-------|------|-------|----|---------------------|-------------------|
| 18 | 580.6 | 30.3 | 723 | 16 | US-11-156-084-18 | Sequence 18, Appl |
| 19 | 578.8 | 30.2 | 720 | 7 | US-10-369-493-38949 | Sequence 38949, A |
| 20 | 578.8 | 30.2 | 720 | 7 | US-10-369-493-38953 | Sequence 38953, A |
| 21 | 578.8 | 30.2 | 720 | 7 | US-10-369-493-38968 | Sequence 38968, A |
| 22 | 577.4 | 30.1 | 723 | 16 | US-11-156-084-16 | Sequence 16, Appl |
| 23 | 577.2 | 30.1 | 2595 | 7 | US-10-369-324-3 | Sequence 3, Appl |
| 24 | 577.2 | 30.1 | 2595 | 7 | US-10-392-301-3 | Sequence 3, Appl |
| 25 | 577.2 | 30.1 | 2595 | 8 | US-10-607-538-3 | Sequence 3, Appl |
| 26 | 577.2 | 30.1 | 2595 | 10 | US-10-667-145-3 | Sequence 3, Appl |
| 27 | 577.2 | 30.1 | 2595 | 10 | US-10-505-079-3 | Sequence 3, Appl |
| 28 | 577.2 | 30.1 | 9323 | 8 | US-10-369-324-4 | Sequence 4, Appl |
| 29 | 577.2 | 30.1 | 9323 | 8 | US-10-607-538-4 | Sequence 4, Appl |
| 30 | 577.2 | 30.1 | 9323 | 10 | US-10-505-079-4 | Sequence 4, Appl |
| 31 | 554.4 | 28.9 | 777 | 7 | US-10-369-493-38971 | Sequence 38971, A |
| 32 | 546.6 | 28.5 | 3183 | 15 | US-10-072-077A-1 | Sequence 1, Appl |
| 33 | 546.6 | 28.5 | 3183 | 15 | US-11-154-865-1 | Sequence 12, Appl |
| 34 | 545.4 | 28.4 | 723 | 6 | US-10-187-339-12 | Sequence 12, Appl |
| 35 | 543.6 | 28.3 | 720 | 7 | US-10-369-493-38936 | Sequence 38936, A |
| 36 | 543.6 | 28.3 | 720 | 7 | US-10-369-493-38940 | Sequence 38940, A |
| 37 | 543.6 | 28.3 | 720 | 7 | US-10-369-493-38964 | Sequence 38964, A |
| 38 | 543.6 | 28.3 | 720 | 7 | US-10-369-493-38966 | Sequence 38966, A |
| 39 | 539.4 | 28.1 | 747 | 6 | US-10-187-339-5 | Sequence 5, Appl |
| 40 | 503.8 | 26.3 | 11746 | 16 | US-11-174-413-75 | Sequence 75, Appl |
| 41 | 503.8 | 26.3 | 11788 | 16 | US-11-174-413-73 | Sequence 73, Appl |
| 42 | 503.8 | 26.3 | 11803 | 16 | US-11-174-413-74 | Sequence 74, Appl |
| 43 | 455 | 23.7 | 559 | 7 | US-10-369-493-37855 | Sequence 37855, A |
| 44 | 305.4 | 15.9 | 2544 | 6 | US-10-187-339-9 | Sequence 9, Appl |
| 45 | 190.6 | 9.9 | 729 | 7 | US-10-369-493-38941 | Sequence 38941, A |

ALIGNMENTS

RESULT 1
US-10-817-483-1
Sequence 1, Application US/10817483
Publication No. US20040237147A1
GENERAL INFORMATION:
APPLICANT: Habben, Jeffrey E.
APPLICANT: Zinselmeier, Christopher
APPLICANT: Tomes, Dwight
APPLICANT: Abdit, Shane
APPLICANT: Helenczaris, Timothy G.
TITLE OF INVENTION: Modulation of Cytokinin Activity in
TITLE OF INVENTION: Plants
FILE REFERENCE: 0803R
CURRENT APPLICATION NUMBER: US/10/817,483
CURRENT FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: US 60/460,718
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 09/545,334
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: US 60/129,844
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1919
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
FEATURE:
NAME/KEY: CDS
LOCATION: (690)...(1411)
OTHER INFORMATION: 1pt
US-10-817-483-1
Query Match 100.0%; Score 1919; DB 9; Length 1919;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1919; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 GGATCCGCTTACAGATTTGCAGCTTTTGAATTTGATTTATGCAATTCGATGCTTT 60
|||||

Db 1 GGATCCGTTACAACTATTCGACGTTTGTAAATTCATATTAATGCAATTCGATGTTT 60
Qy 61 AATAACGAATGTAATGCGTAGAAATATGATTTTATTTATTTATTTATTTATTTG 120
Db 61 AATAACGAATGTAATGCGTAGAAATATGATTTTATTTATTTATTTATTTATTTG 120
Qy 121 AAGTTTGCATTAATGCTAATGTAATTAATAAATTTATGATCTGCGCATTTGTTCA 180
Db 121 AAGTTTGCATTAATGCTAATGTAATTAATAAATTTATGATCTGCGCATTTGTTCA 180
Qy 181 ATGCGCGCTATTCTTCAAAATATCTTGTGATTTTGTTCAGAGCAACAGATGAGAG 240
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Db 241 TAAATTAAGAAGCGCTGTTTGAAGAAATGCTATCATATGTGCCAGCTATAGGCCAT 300
Qy 301 TAAATTCATTTGTAATAGCCGCCCTTATTTGACGCTCATCAATCAATATTAATA 360
Db 301 TAAATTCATTTGTAATAGCCGCCCTTATTTGACGCTCATCAATCAATATTAATA 360
Qy 361 AATATCTCACTCTGTGCGCAGCAATGATGATATTAACGCGAGAAAGTGAAGTAAATGC 420
Db 361 AATATCTCACTCTGTGCGCAGCAATGATGATATTAACGCGAGAAAGTGAAGTAAATGC 420
Qy 421 GGAATAAGCGTCCGAGTGGCATGAAATAGCGCCCTCGCTATTTGCTGATTTAGTCACT 480
Db 421 GGAATAAGCGTCCGAGTGGCATGAAATAGCGCCCTCGCTATTTGCTGATTTAGTCACT 480
Qy 481 ATTGACTTAAGGGTCCCTGTTAGTGAACAATTTGCTTCAAGAGACACCATGCCCC 540
Db 481 ATTGACTTAAGGGTCCCTGTTAGTGAACAATTTGCTTCAAGAGACACCATGCCCC 540
Qy 541 ACACTTTGTTGAAAAACAAGTTGCTTTGGGAAAGAACTTAAGCGCATTTCTCTCAAG 600
Db 541 ACACTTTGTTGAAAAACAAGTTGCTTTGGGAAAGAACTTAAGCGCATTTCTCTCAAG 600
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Db 601 GAGGAATATCGAGGAAGAAATATTAACAGCTCTGTGTAACAGATTTCTTTGCAAAAAT 660
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Db 721 GCACAGGAAGACATCGATGATGCTCTTGGCCAGACAGTGGCTCCCAAGTCTCT 780
Qy 781 CGCTCGATCGGCTCCATGCTGTCTCTCAACTATCAACCGGAAGCGGGGCAACAGATGG 840
Db 781 CGCTCGATCGGCTCCATGCTGTCTCTCAACTATCAACCGGAAGCGGGGCAACAGATGG 840
Qy 841 AAGAACTGAAGGAAGCACTGCTCTGTACTGTGATGATGCGCCCTTTGGTAAAGGTATCA 900
Db 841 AAGAACTGAAGGAAGCACTGCTCTGTACTGTGATGATGCGCCCTTTGGTAAAGGTATCA 900
Qy 901 TTACAGCAAGCAAGCTCATGACGGCTCATTTGCGAGAGTGCACAAATCAGAGGCCAAG 960
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Qy 961 GCGGCTTATTTCTTGAAGGAGATCTATCTGTTGCTCAGGTGATGCGCAAAAGTCTT 1020
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Qy 1081 TCATAGAGGTGGCCAAAGCAGAGTTAAGCAGATGTTAGCGCCCTCTCTGAGGTCTTTCTA 1140
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Qy 1201 TCGATGATATCGATATGAGCCCTGCTATTTGCTACCCAGAACAGATCAGCCGCTATGTC 1260
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Qy 1261 TATTCAGCTCGACGAGATATGAGATTAATTTGATTCACAGGATGCTCAGAGATTTC 1320
Db 1261 TATTCAGCTCGACGAGATATGAGATTAATTTGATTCACAGGATGCTCAGAGATTTC 1320
Qy 1321 TAAATTCAGTGGCGCTGACAGAGACAGAAATTTCCCTTTGTTGGGCGCAGCTTCCAG 1380
Db 1321 TAAATTCAGTGGCGCTGACAGAGACAGAAATTTCCCTTTGTTGGGCGCAGCTTCCAG 1380
Qy 1381 CGTTGAAGGACCACTTTGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 CGTTGAAGGACCACTTTGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Qy 1441 GCTATTTGAATTAAGATGTTGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
Db 1441 GCTATTTGAATTAAGATGTTGCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
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Db 1621 TCAAAATTTAGCAAAAATTTGTTAAAGTCTTTTATGCGGTGAGTGTGCACTTTTCAT 1680
Qy 1681 CATTTGCGCTTAAGAGATTAAGATATTCATATCTGTTAAACCCCGCAGAAATTTAGCG 1740
Db 1681 CATTTGCGCTTAAGAGATTAAGATATTCATATCTGTTAAACCCCGCAGAAATTTAGCG 1740
Qy 1741 TGTGCAATTTAGTTGCGGTTCAACATGATTTTGGCAATAGTGTGTAACCAAGCACTAGC 1800
Db 1741 TGTGCAATTTAGTTGCGGTTCAACATGATTTTGGCAATAGTGTGTAACCAAGCACTAGC 1800
Qy 1801 CAACGTTGCAATATCACTTAATGATGAAACGTTCAAGCTTTCTTCTGAGGCTGCTC 1860
Db 1801 CAACGTTGCAATATCACTTAATGATGAAACGTTCAAGCTTTCTTCTGAGGCTGCTC 1860
Qy 1861 TTGATGATGAGCTCGGCTCTGATTTTAAACCGCGGTTTACGATTAATGACAAAGCTT 1919
Db 1861 TTGATGATGAGCTCGGCTCTGATTTTAAACCGCGGTTTACGATTAATGACAAAGCTT 1919

RESULT 2
US-10-465-008-1
; Sequence 1, Application US/10465008
; Publication No. US2004001616A1
; GENERAL INFORMATION:
; APPLICANT: MANKIN, LUKS S.
; APPLICANT: DA COSTA E SILVA, OSMALDO
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING PLANT PERFORMANCE
; FILE REFERENCE: 16313-0232
; CURRENT APPLICATION NUMBER: US/10/465,008
; PRIOR APPLICATION NUMBER: 2003-06-19
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1997
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens

US-10-465-008-1

Query Match 56.8%; Score 1089.8; DB 8; Length 1997;
Best Local Similarity 84.9%; Pred. No. 9.1e-271;
Matches 1270; Conservative 0; Mismatches 212; Indels 13; Gaps 4;

2 GATCCGGTACAAAGTATGACAGTTTGTGAAATGCGATTTAATGCAATCGATGTTA 61
1 GATCCTGTACAAAGTATGACAGTTTGTGAAATGCGATTTAATGCAATCGATGTTA 60
62 ATAAAGAAATGATAGGCGTA---GAAATATGATTTTATGATTTATCTTCAATG 117
61 ACAAGAAAGTATGCGGTAAGAAAGAAATGATTTATGATTTATGATTTATGAT 120
118 TTGAAGTTTGCATATATATGCTAATGTAATAATTTAAAAATTAATGATGCGCATTTGTT 177
121 TTGAAGTTGCGCATATATGAT-----GTATAGTAAATATATCACTGTCGCAATTATT 174
178 CAAATGGCGCGCTTATTTCAAAAATATCTTTGATTTTGTACAGAGACAGACCTGACAG 237
175 GAAATGGACAGTGTATTTTCAACCATATCTTTGATTTGTGACAAATGACACAGCTGCAAG 234
238 AAGTAAATAAAGACGCTGTTGTGTAAGAAATGCTATCATATGCGCCAGCTATAGGCGC 297
235 AAGTAAATATATGACCGCGTGTGTAAGATTTGCTATCATATGCTTACTATAGGAC 294
298 ATTATAGTTCAATTTGTGAATATGCGCCCTTATTTTGAAGTCTCATCAATCAATATTTA 357
295 ATTATAG-TCATTTGTGAATATGCTGCGCCCTTATTTTGAAGTCTCATCAATATTTA 353
358 AAAATATCTCACTGTCGCGACGAATGATTTAATACCGAGAAAAGTGAGATTAAT 417
354 CAAAGATCTCACTGTCGCGACGAATGATTTAATACCGAGAAAAGTGAGATTTAAG 413
418 CGCGGAAAAACGTCGCGACGATGCGATGATAGCGGCTCCGATTTGCTGATTTAGTCAGC 477
414 CGCGGAAAAACGTCGCGACGATGCGATGATAGCTGCTGCTGATTTGCTGATTTAGTCAGC 473
478 TTTATTTGACTTAAGGGTGCCTCGTTAGTGA CAATTTGCTTTCAAGAGACAGCCATGC 537
474 CTTATTTGACTTAAGGGTGCCTCGTTAGTGA CAATTTGCTTTCAAGAGACAGCCATGC 533
538 CCCACACTTTGTTGAAAAACAAGTTGCTTTTGGGAAAGCACTTAAGCCACTTGCCTTC 597
534 CCCACACTGTTGTTGAAAAACAATTTGCCCTTTTGGGAAAGCACTTAAGCCAGTTGCTTC 593
598 AAGAGGAATATCGAGGAAGAAATATATACAGCCTCTGTAACAGCTTCTCTGTCGAAA 657
594 AATAAGGAATCTCGAGAGGCAATATACCGCCTCTGTAATCACTTCTTAATCCAAA 653
658 AATCAATTTGATTTCAATATTCG--AAGACCGATGATCTACGCTTAATTTTGGCTCC 715
654 AATCAATTTGATTTCAATATTCGCAAAAACCTTAATGATCTGCTTAATTTTGGCTCC 713
716 AACTTGCACAGAAAAGACATGACTGCGATAGCTTTTGGCCAGCAGACTGCGCTCCAGT 775
714 AACTTGCACAGAAAAGACATGACTGCGATAGCTTTTGGCCAGCAGACTGCGCTCCAGT 773
776 CCTCTGCGATGCGCTCAATGCTGCTCAATCTATCAACCGGAAGCGGGCGACCAAC 835
774 CTTTCTGCTGATGCGGCTCAATGCTGCTCAATCTATCAACCGGAAGCGGGCGACCAAC 833
836 AGTGAAGAACTGAAGGAAGACGACTGCTGTAACCTTGAATGATCGCCCTTGGTAAAGG 895
834 AGTGAAGAACTGAAGGAAGACGAGCGCTGTAACCTTGAATGATCGCCCTTGGTAAAGG 893
896 TATCATTTACAGCAAGCAAGCTCATGAACGGCTCATTTGGGAGGCTGCAATCAGAGGC 955
894 TATCATTTACAGCAAGCAAGCTCATGAAGGGCTGATGGGGAGGCTGTAATTAATGAGGC 953
956 CAAAGGCGGGCTTATTTTGAAGGAGATCTATCTGTTGCTCAGATGCAATGAGGCAAG 1015
954 CCAGGCGGGCTTATTTTGAAGGAGATCTATCTGTTGCTCAGATGCAATGAGGCAAG 1013

1016 TCGTATTGGAACCGGATTTTCTGTTGCAATATATGCGAACGAGTTAGCAGACGAGA 1075
1014 CAGTATTGGAAGTGGGATTTTCTGTTGCAATATATGCGAACGAGTTAGCAGACGAGA 1073
1076 GAGCTTCATGAGCGTGGCCAAAGCAGAGTTAAGCAGATGTTACGCGCCCTGCAAGTCT 1135
1074 GAGCTTCATGAGCGTGGCCAAAGCAGAGTTAAGCAGATGTTACGCGCCCTGCAAGTCT 1133
1136 TTTATTTATCCAAAGATTGTTTCACTTTGAGGAGAGCCTCGCTGAGGCCCACTGGA 1195
1134 TTTATTTATCCAAAGATTGTTTCACTTTGAGGAGAGCCTCGCTGAGGCCCACTGGA 1193
1196 AGGATTCAGTGAATATGATATGCGCTGCTATTTGCTACCCGAACAGATCAGCCGGA 1255
1194 AGAGATTCAGTGAATATGATATGCGCTGCTATTTGCTACCCGAACAGATCAGATCCGA 1253
1256 TATGCTATTGCAAGCTCGACGAGATATGAGAAATTAATTGATTCAGCGGATGCTCAGGA 1315
1254 TATGCTATTGCAAGCTCGACGAGATATGAGAAATTAATTGATTCAGCGGATGCTCAGGA 1313
1316 GTTCTTAATCCATGCGCGCTGACAGAAACAGAAATTTCCCTTTGTGGCGCGACAGCTGT 1375
1314 GATCTCATTCATGACGCGCGACAGAAACAGAAATTTCCCTGAGTTAAGCAGCGCTTA 1373
1376 CGAAGCGTTTGAAGCAACCATTTGCAATGATGATATGCAACAGATTTTGTTCAGAC 1435
1374 CGACGGAATTCGAAGGCTCATTCATTCGGAATGATATGATTTGCAACAGCTCCCGTCACAC 1433
1436 TTGTCGCTATTGATTAAGATGCTTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1490
1434 CTGCTTCATTTGAATTAAGATGTTGCAATTTGTTTGTGTTGTTGTTGTTGTTGTTGTTG 1488

RESULT 3
US-10-363-723-2
Sequence 2, Application US/10363723
Publication No. US20040025205A1
GENERAL INFORMATION:
APPLICANT: Agriculture Victoria Services Pty Ltd
APPLICANT: La Trobe University
APPLICANT: SPANGENBERG, German
LIN, Yi Han
APPLICANT: PARISH, Roger W.
APPLICANT: LI, Song Feng W.
APPLICANT: HEAZLEWOOD, Joshua W.
TITLE OF INVENTION: Manipulation of plant senescence
FILE REFERENCE: 14403US
CURRENT APPLICATION NUMBER: US/10/363,723
CURRENT FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: AU PQ9946
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: PCT/AU01/01092
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1988
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
US-10-363-723-2

Query Match 49.9%; Score 956.8; DB 8; Length 1988;
Best Local Similarity 81.4%; Pred. No. 2.4e-236;
Matches 1220; Conservative 0; Mismatches 262; Indels 16; Gaps 9;

1 GGAATCCGTTACAAAGTATGACAGTTTGTGAAATGCGATTTAATGCAATCTGATGTTT 60
1 GGAATCCGTTACAAAGTATGACAGTTTGTGAAATGCGATTTAATGCAATCTGATGTTT 60
61 AATAAGAAATGTAATGGGTGAATATGTAATTTATTTATTTATTTATTTATTTATTTATTTG 120
61 AATAAGAAATGTAATGGGTGAATATGTAATTTATTTATTTATTTATTTATTTATTTATTTG 119

QY 972 CTTGAGGAGATCTATCTCTGTTGCTCAGTGTGATGGCGGAAGTGTATTGGAAACGG 1031
| | | | |
Db 1690 CTTGAGGAGATCTATCTCTGTTGCTCAGTGTGATGGCGGAAGTGTATTGGAAACGG 1749
| | | | |
QY 1032 GATTTTCGTTGAGATATTAATTCGCAACGAGTTAGCAGAGAGAGAGCTTCATGAGCGTG 1091
| | | | |
Db 1750 GATTTTCGTTGAGATATTAATTCGCAACGAGTTAGCAGAGAGAGAGCTTCATGAGCGTG 1809
| | | | |
QY 1092 GCCAAGACCAAGATTAAAGAGATGTTACGCCCTCTGACAGTCTTTCTATTATCCAAAG 1151
| | | | |
Db 1810 GCCAAGACCAAGATTAAAGAGATGTTACGCCCTCTGACAGTCTTTCTATTATCCAAAG 1869
| | | | |
QY 1152 TTGTTCACTTTTGGAGGAGAGCTCGGCTGAGGAGAGAGAGAGAGAGAGAGAGATAT 1211
| | | | |
Db 1870 TTGTTCACTTTTGGAGGAGAGCTCGGCTGAGGAGAGAGAGAGAGAGAGAGATAT 1929
| | | | |
QY 1212 CGATATGCCCTGATATTTGCTATCCAGAACAGATCAGAGAGAGAGAGAGAGAGAGATAT 1271
| | | | |
Db 1930 CGATATGCCCTGATATTTGCTATCCAGAACAGATCAGAGAGAGAGAGAGAGAGATAT 1989
| | | | |
QY 1272 GACGAGATATGAGATTAATTAATGATTCACGGTATCGCTCAGAGAGTTTCTAATCCATGCG 1331
| | | | |
Db 1990 GACGAGATATGAGATTAATTAATGATTCACGGTATCGCTCAGAGAGTTTCTAATCCATGCG 2049
| | | | |
QY 1332 CGTCCAGAGAGACAGAAATTCCTTTGGTGGGCGGACAGCTGTGCAAGCGTTTGAAGA 1391
| | | | |
Db 2050 CGTCCAGAGAGACAGAAATTCCTTTGGTGGGCGGACAGCTGTGCAAGCGTTTGAAGA 2109
| | | | |
QY 1392 CCACCATTTGCAATGTGA 1409
| | | | |
Db 2110 CCACCATTTGCAATGTGA 2127
| | | | |

RESULT 5
US-11-139-461-8

Sequence 8, Application US/11139461
Publication No. US20050229274A1
GENERAL INFORMATION:
APPLICANT: Zinselmeyer, Chris
APPLICANT: Haben, Jeff
APPLICANT: Tomes, Dwight
TITLE OF INVENTION: Regulated Expression of Genes in Plant
TITLE OF INVENTION: Seeds
FILE REFERENCE: 0803
CURRENT APPLICATION NUMBER: US/11/139,461
CURRENT FILING DATE: 2005-05-27
PRIOR APPLICATION NUMBER: US 60/129,844
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 2722
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter from Hordeum vulgare, Plant Journal 6:849-860
OTHER INFORMATION: (1994); gene from Agrobacterium tumefaciens, Molecular
OTHER INFORMATION: and General Genetics 216:388-394 (1989); terminator
OTHER INFORMATION: from Zea mays, Genbank Accession #S78780.
US-11-139-461-8

Query Match 37.5%; Score 720.4; DB 13; Length 2722;
Best Local Similarity 99.9%; Pred. No. 4,6e-175;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 668 CGATGATCTACGTCCTAATTTTCGGTCCACTTTCGACAGAGAAAGACATGATCGCATG 747
| | | | |
Db 1523 CGATGATCTACGTCCTAATTTTCGGTCCACTTTCGACAGAGAAAGACATGATCGCATG 1582
| | | | |
QY 748 CTTTGGCCAG 807
| | | | |
Db 1583 CTTTGGCCAG 1642
| | | | |

QY 808 AACTATCAACCGGAAGCGGGGCGACCAACGATGGAAGAACTGAAAGGAAGCACTGCTGT 867
| | | | |
Db 1643 AACTATCAACCGGAAGCGGGGCGACCAACGATGGAAGAACTGAAAGGAAGCACTGCTGT 1702
| | | | |
QY 868 ACCGTGATATGAG 927
| | | | |
Db 1703 ACCGTGATATGAG 1762
| | | | |
QY 928 TCATTCGAGAGGTGCAACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 987
| | | | |
Db 1763 TCATTCGAGAGGTGCAACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1822
| | | | |
QY 988 TCTCGTGTCTGAGGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1047
| | | | |
Db 1823 TCTCGTGTCTGAGGTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1882
| | | | |
QY 1048 TTATTCGCAACGAGTTAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1107
| | | | |
Db 1883 TTATTCGCAACGAGTTAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1942
| | | | |
QY 1108 AGCAGATGTTAAGCGCCCTCTGAGAGTCTTTCTATTATCCAAAGTTGTTCACTTTGGA 1167
| | | | |
Db 1943 AGCAGATGTTAAGCGCCCTCTGAGAGTCTTTCTATTATCCAAAGTTGTTCACTTTGGA 2002
| | | | |
QY 1168 GGAAGCTTGGCTGAT 1227
| | | | |
Db 2003 GGAAGCTTGGCTGAT 2062
| | | | |
QY 1228 TTGCTAACCGAGAACAGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1287
| | | | |
Db 2063 TTGCTAACCGAGAACAGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2122
| | | | |
QY 1288 ATAAATGATTCACGATATGCTCAGAGAGTTTCTAATCCATGAGAGAGAGAGAGAGAG 1347
| | | | |
Db 2123 ATAAATGATTCACGATATGCTCAGAGAGTTTCTAATCCATGAGAGAGAGAGAGAGAG 2182
| | | | |
QY 1348 AATTCCTTTGGTGGGCGGACAGAGCTGTGGAAGCGTTTGAAGAGACCACTTTGGAATG 1407
| | | | |
Db 2183 AATTCCTTTGGTGGGCGGACAGAGCTGTGGAAGCGTTTGAAGAGACCACTTTGGAATG 2242
| | | | |
QY 1408 GA 1409
| | | | |
Db 2243 GA 2244
| | | | |

RESULT 6
US-11-139-461-9

Sequence 9, Application US/11139461
Publication No. US20050229274A1
GENERAL INFORMATION:
APPLICANT: Zinselmeyer, Chris
APPLICANT: Haben, Jeff
APPLICANT: Tomes, Dwight
TITLE OF INVENTION: Regulated Expression of Genes in Plant
TITLE OF INVENTION: Seeds
FILE REFERENCE: 0803
CURRENT APPLICATION NUMBER: US/11/139,461
CURRENT FILING DATE: 2005-05-27
PRIOR APPLICATION NUMBER: US 60/129,844
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 2722
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Promoter from Zea mays, U.S. patent application 09/377,648;
OTHER INFORMATION: gene from Agrobacterium tumefaciens, Molecular and General
OTHER INFORMATION: Genetics 216:388-394 (1989); terminator from Solanum
OTHER INFORMATION: tuberosum, Plant Cell 1(1):115-122 (1989).
US-11-139-461-9

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Query Match      37.5% Score 720.4; DB 13; Length 2722;
Best Local Similarity 99.9%; Pred. No. 4.6e-175;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 688 CGATGATCTACGCTAATTTTCCGATCCAACTTGACAGAGAAGACATGACGTGGATAG 747
DB 1523 CCATGGATCTACGCTAATTTTCCGATCCAACTTGACAGAGAAGACATGACGTGGATAG 1582
QY 748 CTCTTGGCCAGACAGCTGGCCCTCCAGTCTCTGCTGATGCGGTCCAAATGCTGTCTC 807
DB 1583 CTCTTGGCCAGACAGCTGGCCCTCCAGTCTCTGCTGATGCGGTCCAAATGCTGTCTC 1642
QY 808 AACTATCAACCGGAAGCGGGGAGCCAAAGTGGAAGAACTGAAGGAAGCACTGCTCTGT 867
DB 1643 AACTATCAACCGGAAGCGGGGAGCCAAAGTGGAAGAACTGAAGGAAGCACTGCTCTGT 1702
QY 868 ACCTTGATGATGCGCCCTTTGGTAAAGGGTATCATTTACAGCCAGCAAGCACTGATGAACGGC 927
DB 1703 ACCTTGATGATGCGCCCTTTGGTAAAGGGTATCATTTACAGCCAGCAAGCACTGATGAACGGC 1762
QY 928 TCATTGCGGAGGTGACAAATCAAGAGCCAAAGCGGCTTATTTTGAAGGAGATCTA 987
DB 1763 TCATTGCGGAGGTGACAAATCAAGAGCCAAAGCGGCTTATTTTGAAGGAGATCTA 1822
QY 988 TCTGCTGCTCAGGTCATGAGTGCGCAAGTCTTATTGGAAGCGGATTTTGGTGGCATTA 1047
DB 1823 TCTGCTGCTCAGGTCATGAGTGCGCAAGTCTTATTGGAAGCGGATTTTGGTGGCATTA 1882
QY 1048 TTATTTCGCAACGAGTTTACAGACAGAGAGCTTCATGAGCGTGCCAAAGCAGAGTTTA 1107
DB 1883 TTATTTCGCAACGAGTTTACAGACAGAGAGCTTCATGAGCGTGCCAAAGCAGAGTTTA 1942
QY 1108 AGCAGATGTTACGCCCCCTCTGCAAGTCTTTTCTATTATCAAGAGTTGGTTCACATTTGGA 1167
DB 1943 AGCAGATGTTACGCCCCCTCTGCAAGTCTTTTCTATTATCAAGAGTTGGTTCACATTTGGA 2002
QY 1168 GGGAGCCTCGGCTGAGGCCCAATCTGGAAGGGATGATGATGATGATGATGATGATGATGAT 1227
DB 2003 GGGAGCCTCGGCTGAGGCCCAATCTGGAAGGGATGATGATGATGATGATGATGATGATGAT 2062
QY 1228 TTGCTACCCAGAACAGATCAAGCCCGATATGCTATTGCACTGCAAGCAGATATGAGA 1287
DB 2063 TTGCTACCCAGAACAGATCAAGCCCGATATGCTATTGCACTGCAAGCAGATATGAGA 2122
QY 1288 ATAAATGATTCACGCTATCGCTCAGAGTTTCTAATCCATGCGGTGACAGAAACGA 1347
DB 2123 ATAAATGATTCACGCTATCGCTCAGAGTTTCTAATCCATGCGGTGACAGAAACGA 2182
QY 1348 AATTCCCTTTGGTGGGCGGACAGCTGTGGAAGCGTTTGAAGGACCAACATTTGCAATGT 1407
DB 2183 AATTCCCTTTGGTGGGCGGACAGCTGTGGAAGCGTTTGAAGGACCAACATTTGCAATGT 2242
QY 1408 GA 1409
DB 2243 GA 2244

RESULT 7
US-11-139-461-7
; Sequence 7, Application US/11139461
; Publication No. US20050229274A1
; GENERAL INFORMATION:
; APPLICANT: Zinsemeister, Chris
; APPLICANT: Haben, Jeff
; APPLICANT: Tomes, Dwight
; TITLE OF INVENTION: Regulated Expression of Genes in Plant
; FILE REFERENCE: 0803
; CURRENT APPLICATION NUMBER: US/11/139,461
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/129,844
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 12
```

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SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 5622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Promoter and terminator from Zea mays as found in
; OTHER INFORMATION: Genbank Accession #578780; gene from Agrobacterium
; OTHER INFORMATION: tumefaciens as found in Molecular and General
; OTHER INFORMATION: Genetics 216:388-394 (1989).
US-11-139-461-7

Query Match      37.5% Score 720.4; DB 13; Length 5622;
Best Local Similarity 99.9%; Pred. No. 6.8e-175;
Matches 721; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 688 CGATGATCTACGCTAATTTTCCGATCCAACTTGACAGAGAAGACATGACGTGGATAG 747
DB 1523 CCATGGATCTACGCTAATTTTCCGATCCAACTTGACAGAGAAGACATGACGTGGATAG 1582
QY 748 CTCTTGGCCAGACAGCTGGCCCTCCAGTCTCTGCTGATGCGGTCCAAATGCTGTCTC 807
DB 1583 CTCTTGGCCAGACAGCTGGCCCTCCAGTCTCTGCTGATGCGGTCCAAATGCTGTCTC 1642
QY 808 AACTATCAACCGGAAGCGGGGAGCCAAAGTGGAAGAACTGAAGGAAGCACTGCTCTGT 867
DB 1643 AACTATCAACCGGAAGCGGGGAGCCAAAGTGGAAGAACTGAAGGAAGCACTGCTCTGT 1702
QY 868 ACCTTGATGATGCGCCCTTTGGTAAAGGGTATCATTTACAGCCAGCAAGCACTGATGAACGGC 927
DB 1703 ACCTTGATGATGCGCCCTTTGGTAAAGGGTATCATTTACAGCCAGCAAGCACTGATGAACGGC 1762
QY 928 TCATTGCGGAGGTGACAAATCAAGAGCCAAAGCGGCTTATTTTGAAGGAGATCTA 987
DB 1763 TCATTGCGGAGGTGACAAATCAAGAGCCAAAGCGGCTTATTTTGAAGGAGATCTA 1822
QY 988 TCTGCTGCTCAGGTCATGAGTGCGCAAGTCTTATTGGAAGCGGATTTTGGTGGCATTA 1047
DB 1823 TCTGCTGCTCAGGTCATGAGTGCGCAAGTCTTATTGGAAGCGGATTTTGGTGGCATTA 1882
QY 1048 TTATTTCGCAACGAGTTTACAGACAGAGAGCTTCATGAGCGTGCCAAAGCAGAGTTTA 1107
DB 1883 TTATTTCGCAACGAGTTTACAGACAGAGAGCTTCATGAGCGTGCCAAAGCAGAGTTTA 1942
QY 1108 AGCAGATGTTACGCCCCCTCTGCAAGTCTTTTCTATTATCAAGAGTTGGTTCACATTTGGA 1167
DB 1943 AGCAGATGTTACGCCCCCTCTGCAAGTCTTTTCTATTATCAAGAGTTGGTTCACATTTGGA 2002
QY 1168 GGGAGCCTCGGCTGAGGCCCAATCTGGAAGGGATGATGATGATGATGATGATGATGATGAT 1227
DB 2003 GGGAGCCTCGGCTGAGGCCCAATCTGGAAGGGATGATGATGATGATGATGATGATGATGAT 2062
QY 1228 TTGCTACCCAGAACAGATCAAGCCCGATATGCTATTGCACTGCAAGCAGATATGAGA 1287
DB 2063 TTGCTACCCAGAACAGATCAAGCCCGATATGCTATTGCACTGCAAGCAGATATGAGA 2122
QY 1288 ATAAATGATTCACGCTATCGCTCAGAGTTTCTAATCCATGCGGTGACAGAAACGA 1347
DB 2123 ATAAATGATTCACGCTATCGCTCAGAGTTTCTAATCCATGCGGTGACAGAAACGA 2182
QY 1348 AATTCCCTTTGGTGGGCGGACAGCTGTGGAAGCGTTTGAAGGACCAACATTTGCAATGT 1407
DB 2183 AATTCCCTTTGGTGGGCGGACAGCTGTGGAAGCGTTTGAAGGACCAACATTTGCAATGT 2242
QY 1408 GA 1409
DB 2243 GA 2244

RESULT 8
US-10-409-701-2
; Sequence 2, Application US/10409701
; Publication No. US2003022124A1
```

GENERAL INFORMATION:
APPLICANT: Zinselmeier, Chris
TITLE OF INVENTION: Enhanced Silk Exsersion Under Stress
FILE REFERENCE: 1421
CURRENT APPLICATION NUMBER: US/10/409,701
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: US 60/370,796
PRIOR FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 723
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(720)
US-10-409-701-2

Query Match 37.5%; Score 720; DB 7; Length 723;
Best Local Similarity 100.0%; Pred. No. 2.8e-175;

Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 ATGATCTACGCTCTAATTTTGGGTCCAACTTGACAGGAAAGACATCGACTGCCATAGCT 749
DB 1 ATGATCTACGCTCTAATTTTGGGTCCAACTTGACAGGAAAGACATCGACTGCCATAGCT 60
QY 750 CTTGCCAGACAGACTGGGCTCCCACTCTGCTCGATCGCGTCCAAAGCTGTCTCAA 809
DB 61 CTTGCCAGACAGACTGGGCTCCCACTCTGCTCGATCGCGTCCAAAGCTGTCTCAA 120
QY 810 CTATCAACCGGAAGCGGGGCAACAGTGAAGAAGCTGAAGAAAGCACTGTCTGTAC 869
DB 121 CTATCAACCGGAAGCGGGGCAACAGTGAAGAAGCTGAAGAAAGCACTGTCTGTAC 180
QY 870 CTTGATGATCGCCCTTTTGGTAAAGGATCATTAAGCCAGCAAGCTCATGAAGCGCTC 929
DB 181 CTTGATGATCGCCCTTTTGGTAAAGGATCATTAAGCCAGCAAGCTCATGAAGCGCTC 240
QY 930 ATTGGGAGGAGTGCACAAATCAAGAGCCAAAGCGGGCTTATCTTGAAGGAGATCTATC 989
DB 241 ATTGGGAGGAGTGCACAAATCAAGAGCCAAAGCGGGCTTATCTTGAAGGAGATCTATC 300
QY 990 TCGTTGCTCAGGTGATGAGCGCAAGTGTATTGGAACGCGGATTTTCTGTGCGATATT 1049
DB 301 TCGTTGCTCAGGTGATGAGCGCAAGTGTATTGGAACGCGGATTTTCTGTGCGATATT 360
QY 1050 ATTGCGAAGAGTATGACAGAGAGAGAGCTTCATGAGCGTGGCCAAAGCCAGAGTTAAG 1109
DB 361 ATTGCGAAGAGTATGACAGAGAGAGAGCTTCATGAGCGTGGCCAAAGCCAGAGTTAAG 420
QY 1110 CAGATGTTACCGCCCTCTGCAAGTCTTCTATTATCAAGAGTGGTCAACTTTGGAGG 1169
DB 421 CAGATGTTACCGCCCTCTGCAAGTCTTCTATTATCAAGAGTGGTCAACTTTGGAGG 480
QY 1170 GAGCCTCGGCTGAGGCGCCATCTGGAAGGAGATCGATGATATCGATATGCCCTGTATT 1229
DB 481 GAGCCTCGGCTGAGGCGCCATCTGGAAGGAGATCGATGATATCGATATGCCCTGTATT 540
QY 1230 GCTACCCGAAACAGATACGCGCGATATGCTATTGAGCTTCGACGCGAGATATGAGAGAT 1289
DB 541 GCTACCCGAAACAGATACGCGCGATATGCTATTGAGCTTCGACGCGAGATATGAGAGAT 600
QY 1290 AAATGATTCACGAGTATGCTCAGAGTTTCTAATCCATCGCGCGTGCAGAGAAAGAAA 1349
DB 601 AAATGATTCACGAGTATGCTCAGAGTTTCTAATCCATCGCGCGTGCAGAGAAAGAAA 660
QY 1350 TTCCCTTTGGTGGGCGCAGAGCTGTCAAGCGTTTGAAGACCAACATTTGGAATGTGA 1409
DB 661 TTCCCTTTGGTGGGCGCAGAGCTGTCAAGCGTTTGAAGACCAACATTTGGAATGTGA 720

RESULT 9

US-10-369-493-38935

Sequence 38935, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xiandeng

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 38935

LENGTH: 717

TYPE: DNA

ORGANISM: Agrobacterium tumefaciens

US-10-369-493-38935

Query Match 37.4%; Score 717; DB 7; Length 717;
Best Local Similarity 100.0%; Pred. No. 1.7e-174;

Matches 717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 690 ATGATCTACGCTCTAATTTTGGGTCCAACTTGACAGGAAAGACATCGACTGCCATAGCT 749
DB 1 ATGATCTACGCTCTAATTTTGGGTCCAACTTGACAGGAAAGACATCGACTGCCATAGCT 60
QY 750 CTTGCCAGACAGACTGGGCTCCCACTCTGCTCGATCGCGTCCAAAGCTGTCTCAA 809
DB 61 CTTGCCAGACAGACTGGGCTCCCACTCTGCTCGATCGCGTCCAAAGCTGTCTCAA 120
QY 810 CTATCAACCGGAAGCGGGGCAACAGTGAAGAAGCTGAAGAAAGCACTGTCTGTAC 869
DB 121 CTATCAACCGGAAGCGGGGCAACAGTGAAGAAGCTGAAGAAAGCACTGTCTGTAC 180
QY 870 CTTGATGATCGCCCTTTTGGTAAAGGATCATTAAGCCAGCAAGCTCATGAAGCGGCTC 929
DB 181 CTTGATGATCGCCCTTTTGGTAAAGGATCATTAAGCCAGCAAGCTCATGAAGCGGCTC 240
QY 930 ATTGGGAGGAGTGCACAAATCAAGAGCCAAAGCGGGCTTATCTTGAAGGAGATCTATC 989
DB 241 ATTGGGAGGAGTGCACAAATCAAGAGCCAAAGCGGGCTTATCTTGAAGGAGATCTATC 300
QY 990 TCGTTGCTCAGGTGATGAGCGCAAGTGTATTGGAACGCGGATTTTCTGTGCGATATT 1049
DB 301 TCGTTGCTCAGGTGATGAGCGCAAGTGTATTGGAACGCGGATTTTCTGTGCGATATT 360
QY 1050 ATTGCGAAGAGTATGACAGAGAGAGAGCTTCATGAGCGTGGCCAAAGCCAGAGTTAAG 1109
DB 361 ATTGCGAAGAGTATGACAGAGAGAGAGCTTCATGAGCGTGGCCAAAGCCAGAGTTAAG 420
QY 1110 CAGATGTTACCGCCCTCTGCAAGTCTTCTATTATCAAGAGTGGTCAACTTTGGAGG 1169
DB 421 CAGATGTTACCGCCCTCTGCAAGTCTTCTATTATCAAGAGTGGTCAACTTTGGAGG 480
QY 1170 GAGCCTCGGCTGAGGCGCCATCTGGAAGGAGATCGATGATATCGATATGCCCTGTATT 1229
DB 481 GAGCCTCGGCTGAGGCGCCATCTGGAAGGAGATCGATGATATCGATATGCCCTGTATT 540
QY 1230 GCTACCCGAAACAGATACGCGCGATATGCTATTGAGCTTCGACGCGAGATATGAGAGAT 1289
DB 541 GCTACCCGAAACAGATACGCGCGATATGCTATTGAGCTTCGACGCGAGATATGAGAGAT 600
QY 1290 AAATGATTCACGAGTATGCTCAGAGTTTCTAATCCATCGCGCGTGCAGAGAAAGAAA 1349
DB 601 AAATGATTCACGAGTATGCTCAGAGTTTCTAATCCATCGCGCGTGCAGAGAAAGAAA 660
QY 1350 TTCCCTTTGGTGGGCGCAGAGCTGTCAAGCGTTTGAAGACCAACATTTGGAATG 1406

Db 361 ATTGCCACGAGTTAGCAGACGAGAGACCTTCATGAACTGTGCCAAGCCAGAGTTAAG 420
Qy 1110 CAGATGTTACGCCCTCTGCGAGGTCTTCTATTAATCCAAAGTGGTTCAACTTTGAGG 1169
Db 421 CAGATGTTACGCCCTCTGCGAGGCTTTCTATTAATCCAAAGAGTGGTTGATCTTTGAGAA 480
Qy 1170 GAGCGTGGCTGAGAGCCCATCTAGTAAGAGATTCAGATGATTCGATATGCTGCTATTT 1229
Db 481 GAGCGTGGCTGAGAGCCCATCTAGTAAGAGATTCAGATGATTCGATATGCTGCTATTT 540
Qy 1230 GCTACCCGAGAACCAAGATCACGCCCGATATGCTATTCAGCTCGACGAGATATGAGAT 1289
Db 541 GCTACCCGAGAACCAAGATCACATCCGATATGCTATTCAGCTTCGACGAGATATGAGAGAT 600
Qy 1290 AAATGATTCACGATATGCTCAGAGATTTCTAATCCATGCGCGTTCGACAGAAACAGAA 1349
Db 601 AAGTTGATTCATGGAGATGCTCAGAGATATCTCATCCATGCAACGCGCAAGAACAGAAA 660
Qy 1350 TTCCCTTGGTGGGCGCAGACGCTGTGAGAGGTTGAAGACCACTTTGGAATGT 1407
Db 661 TTCCCTCGAGTTAACGACGCCGCTTAGCAGGATTCGAAGTTCATCCATTGGAATGT 718

RESULT 14

US-11-156-084-1
; Sequence 1, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(723)
US-11-156-084-1

Query Match 30.3%; Score 582.2; DB 16; Length 723;
Best Local Similarity 87.8%; Pred. No. 1.3e-139;
Matches 635; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 690 ATGATCTACGCTTAATTTTGGTCCAACTTGACAGAGAAAGACATGCACTGCATGACT 749
Db 1 ATGATCTACGCTTAATTTTGGTCCAACTTGACAGAGAAAGACATGCACTGCATGACT 60
Qy 750 CTTGCCAGCAGACTGGCTCCCAATCCTCTCGCTCGATTCGCTCAATGCTGTCTCAA 809
Db 61 CTTGCCAGCAGACTGGCTCCCAATCCTCTCGCTCGATTCGCTCAATGCTGTCTCAA 120
Qy 810 CTATCAACCGGAACGGGCGACCAACAGTGAAGAACTGAAAGAAAGCACTCGTCTGAC 869
Db 121 CTGTCAACCGGAACGGGCGACCAACAGTGAAGAACTGAAAGAAAGCACTCGTCTAATC 180
Qy 870 CTTGATATGCGCCCTTTGGTAAAGGATCATTAACAGCAAGCAAGCTCATGAACGCTC 929
Db 181 CTTGATATGCGCCCTCTGTGTAAAGGATCATTCGACAGCAAGCAAGCTCATGAAGGCTG 240
Qy 930 ATTGCGAGGTGCAACAATCAGAGCCCAAGCGCGGCTTAATCTTGAAGAGATCTATC 989
Db 241 ATTGCGAGGTGATTAATTAATTAAGGCCCAAGCGCGGCTTAATCTTGAAGAGATCTATC 300
Qy 990 TCGTTGCTCAGGTGATGAGCCCAAGTGTATTGGAACGGGATTTTCTGTGCAATTT 1049
Db 301 TCGTTGCTCAGGTGATGAGCCCAAGTGTATTGGAAGTGTGCAATTTTCTGTGCAATTT 360

Qy 1050 ATTGCCACGAGTTAGCAGACGAGAGACTTCATGAGCTGTGCCAAGCCAGAGTTAAG 1109
Db 361 ATTGCCACGAGTTAGCAGACGAGAGACTTCATGAACTGTGCCAAGCCAGAGTTAAG 420
Qy 1110 CAGATGTTACGCCCTCTGCGAGGTCTTCTAATTAATCCAAAGTGGTTCAACTTTGAGG 1169
Db 421 CAGATGTTACGCCCTCTGCGAGGCTTTCTATTAATCCAAAGAGTGGTTGATCTTTGAGAA 480
Qy 1170 GAGCGTGGCTGAGAGCCCATCTAGTAAGAGATTCAGATGATTCGATATGCTGCTATTT 1229
Db 481 GAGCGTGGCTGAGAGCCCATCTAGTAAGAGATTCAGATGATTCGATATGCTGCTATTT 540
Qy 1230 GCTACCCGAGAACCAAGATCACGCCCGATATGCTATTCAGCTCGACGAGATATGAGAT 1289
Db 541 GCTACCCGAGAACCAAGATCACATCCGATATGCTATTCAGCTTCGACGAGATATGAGAGAT 600
Qy 1290 AAATGATTCACGATATGCTCAGAGATTTCTAATCCATGCGCGTTCGACAGAAACAGAA 1349
Db 601 AAGTTGATTCATGGAGATGCTCAGAGATATCTCATCCATGCAACGCGCAAGAACAGAAA 660
Qy 1350 TTCCCTTGGTGGGCGCAGACGCTGTGAGAGGTTGAAGACCACTTTGGAATGTGA 1409
Db 661 TTCCCTCGAGTTAACGACGCCGCTTAGCAGGATTCGAAGTTCATCCATTGGAATGTAT 720

RESULT 15

US-11-156-084-20
; Sequence 20, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(723)
US-11-156-084-20

Query Match 30.3%; Score 582.2; DB 16; Length 723;
Best Local Similarity 87.8%; Pred. No. 1.3e-139;
Matches 635; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 690 ATGATCTACGCTTAATTTTGGTCCAACTTGACAGAGAAAGACATGCACTGCATGACT 749
Db 1 ATGATCTACGCTTAATTTTGGTCCAACTTGACAGAGAAAGACATGCACTGCATGACT 60
Qy 750 CTTGCCAGCAGACTGGCTCCCAATCCTCTCGCTCGATTCGCTCAATGCTGTCTCAA 809
Db 61 CTTGCCAGCAGACTGGCTCCCAATCCTCTCGCTCGATTCGCTCAATGCTGTCTCAA 120
Qy 810 CTATCAACCGGAACGGGCGACCAACAGTGAAGAACTGAAAGAAAGCACTCGTCTGAC 869
Db 121 CTGTCAACCGGAACGGGCGACCAACAGTGAAGAACTGAAAGAAAGCACTCGTCTAATC 180
Qy 870 CTTGATATGCGCCCTTTGGTAAAGGATCATTAACAGCAAGCAAGCTCATGAACGCTC 929
Db 181 CTTGATATGCGCCCTCTGTGTAAAGGATCATTCGACAGCAAGCAAGCTCATGAAGGCTG 240
Qy 930 ATTGCGAGGTGCAACAATCAGAGCCCAAGCGCGGCTTAATCTTGAAGAGATCTATC 989


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Db      241 ATGGGGGGGTATATATATGAGGCCACGGGGCTTATCTTGAGGAGATCTATC 300
Oy      990 TCGTTGCTCAGGTGCAATGCGGAAAATCGTAAATGGAAACGCGAATTTTGGTGCATATT 1049
Db      301 TCGTGTCTCAAGTCATGGCGCAAGCAGTTATGGAGTGGGATTTTCTTGGCATATT 360
Oy      1050 ATTGCCAAGAGTTAGCAGACGAGAGAGCTTCATGAGCGTGGCCAAAGCAGAGTTAAG 1109
Db      361 ATTGCCAAGAGTTAGCAGACGAGAGAGCTTCATGAGCGTGGCCAAAGCAGAGTTAAG 420
Oy      1110 CAGATGTACGCGCCCTGTCAGAGTCTTCTATTTATCCAAAGAGTTGGTTCACTTTGAGG 1169
Db      421 CAGATGTACGCGCCCTGTCAGAGTCTTCTATTTATCCAAAGAGTTGGTTCACTTTGAGG 480
Oy      1170 GAGCCTCGGCTGAGGCCCATACCTGGAAGGATCGATGATATGATATGCCCTGCTATT 1229
Db      481 GAGCCTCGGCTGAGGCCCATACCTGGAAGGATCGATGATATGATATGCCCTGCTATT 540
Oy      1230 GCTACCCGAACCAATACAGCCCGATATGCTATTGCACTGACCGCAGATATGAGAAAT 1289
Db      541 GCTACCCGAACCAATACAGCCCGATATGCTATTGCACTGACCGCAGATATGAGAAAT 600
Oy      1290 AAATGATTCACGATATGCTCAGAGTTTCTAATCCATGCGGTCGACAGAACAGAAA 1349
Db      601 AAATGATTCACGATATGCTCAGAGTTTCTAATCCATGCGGTCGACAGAACAGAAA 660
Oy      1350 TTCCCTTGTGGGCGCAGACAGCTGTGAAAGCGTTGAAGAACCAATTTGAAATGTA 1409
Db      661 TTCCCTGAGTTAAACGACGCGCTTACGACGATTCGAAGTCATTCGAAATGTAT 720
Oy      1410 TAG 1412
Db      721 TAG 723
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Search completed: June 26, 2006, 20:38:39
Job time : 2434 secs

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; Sequence 766, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOCKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: Proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 766
; LENGTH: 7001
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-517-441-766
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Query Match          2.2%; Score 42.6; DB 6; Length 7001;
Best Local Similarity 48.5%; Pred. No. 0.063;
Matches 117; Conservative 0; Mismatches 124; Indels 0; Gaps 0;
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QY 1405 TGTGATAGATTGCACGATTTTGTTCAGACTTGCTATTGTAATAGATGTCGTTTC 1464
    |||||
DB 6641 TGGGATTTAGCATGAGTTGGGTTTGAATATTAGATTTAATGATTTTGG 6700
QY 1465 TTTGTTGCTGCTGCTGTTGATAGAGCAAGTGTGGAACCTGTTTACTGCTTT 1524
    |||||
DB 6701 TTTTAATTTTGGGTTTATTTTATTTGATAGTGTGGTTTGTATGTTAGTTT 6760
QY 1525 ATTTCAGTCTCTGGACGATGTTTCAATATATATTTGAAAATTGCTTTTATA 1584
    |||||
DB 6761 ATTTTATGTAATATAAAGTGCTTTAGTAATATTTAGTAAATTTTAATA 6820
QY 1585 TTCTAGAACGAATTAATGTAAGTATAGCCGTTATCAAAATTTAGCAAAAATGTTAA 1644
    |||||
DB 6821 TTATTTGTAATATAAAGGTAATTAATAGTATTTAGAAAGATGTAAGTTTATA 6880
QY 1645 A 1645
DB 6881 A 6881
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RESULT 10

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US-10-517-441-724
; Sequence 724, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOCKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
```

```
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast c
; TITLE OF INVENTION: Proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 724
; LENGTH: 11021
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-517-441-724
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Query Match          2.2%; Score 42.6; DB 6; Length 11021;
Best Local Similarity 47.7%; Pred. No. 0.078;
Matches 155; Conservative 0; Mismatches 169; Indels 1; Gaps 1;
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QY 1384 TTGAAGACCAACATTTGGAATGATGATGACCAAGTTTGTTCAGACTTTCGCT 1443
    |||||
DB 473 TTTGATTAAGAAATATTTAAATTTGTTTAAATTTTAAATTTTGTGAGCTTTATTT 532
QY 1444 ATTGAATAGATGTCCTCT-TTGTGCTGCTGCTGCTGATAGAGCAAGTGTTC 1502
    |||||
DB 533 ATATGATATAAATTTTGGTTTATTTATTTTATTTTAAATTTAGATATTTTAAGTTT 592
QY 1503 TGAACCTGTTTATTCAGCTTATTTTCACTCTTGACAGATGTTTACAAATTAATA 1562
    |||||
DB 593 AGATTAATTAATTTTATTTTAAATTTGTAATTTAGAAAATTTTGAATTTATTTAG 652
QY 1563 TTGCAAAATTTGCTTTTATATTCGTAGAACGAATTAATGTAAGTATGCCCTTATC 1622
    |||||
DB 653 ATTGGAAGTTTGGTTTATGTTTATTTTATTTTATTTTATTTTAAATTTAATTTT 712
QY 1623 AAAATTTAGCAAAAATTTGTAAGGTTCTTTATGCGGTGAGTTGCGACTTTTCATCA 1682
    |||||
DB 713 TATGATTTGATGATGTTTATTTATTTTATTTTAAATGATATTTAGTTGTTTAAATTA 772
QY 1683 TTGTCGCTAAGAGTTACGATAT 1707
DB 773 TTTTGGTATATGTTTATTTAGGTTT 797
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RESULT 11

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US-10-517-441-310
; Sequence 310, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOCKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
```



```

? APPLICANT: SCHMITT, Manfred
? APPLICANT: LOOK, Maxime P.
? APPLICANT: MARX, Almut
? APPLICANT: HOEFLE, Heinz
? TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast ce
? TITLE OF INVENTION: Proliferative disorders
? FILE REFERENCE: 47675-93
? CURRENT APPLICATION NUMBER: US/10/517,441
? CURRENT FILING DATE: 2004-12-11
? PRIOR APPLICATION NUMBER: PCT/EP2003/010861
? PRIOR FILING DATE: 2003-10-01
? PRIOR APPLICATION NUMBER: DE 10317955.0
? PRIOR FILING DATE: 2003-04-17
? PRIOR APPLICATION NUMBER: DE 10300096.8
? PRIOR FILING DATE: 2003-01-07
? PRIOR APPLICATION NUMBER: DE 10245779.4
? PRIOR FILING DATE: 2002-10-01
? NUMBER OF SEQ ID NOS: 2147
? SEQ ID NO 310
? LENGTH: 6521
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
? US-10-517-441-310

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Query Match      2.2%; Score 42.2; DB 6; Length 6521;
Beet Local Similarity 49.3%; Pred. No. 0.078;
Matches 110; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

OY      1423 TTTTGTTCAACACTGTTCGCTATTGTAATAAGATGTCCTTGTGTGTGGTGCT 1482
DB      4945 TTATTGTTTAAAGGTTTGTAGTTTATAAAGGAGAGGTCGTATTGATTGAGTTAGT 5004

OY      1483 TGTGATAGAGCAAGTGGTTGAAACTGTTTACTGCTTATTTTCACTCTTGAC 1542
DB      5005 TTTTATTATTAATAGTATATATGAGCTTTTGGTTATTTTGTAAATATAGATTGTTGGAG 5064

OY      1543 GATGTTTACAAATATATAATTATGTGAAAAATGTGGTTTATATTCGTGAGCAAAATPAA 1602
DB      5065 GTTAAAGTAGTAGAGAGAGATTGTTGAGGTTAGAGAGTTTAAAAATTAGTTGAGTAAATATAG 5124

OY      1603 TGTGTAAGTATAGCCGTTATCAAAAATTAGCAAAAATTGTTAAA 1645
DB      5125 TGAGATTTTATTATTATTATTAATAAAATTAATAAAATAGTAGA 5167

RESULT 12
US-10-517-441-584
; Sequence 584, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MATER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMIRICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARK, Almut
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cancer
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0

```

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; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 584
; LENGTH: 6521
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-584

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[illegible]

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RESULT 13
US-10-517-441-538
; Sequence 538, Application US/10517441
; Publication No. US20060121467a1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almut
; APPLICANT: HOEFLE, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast ce
; TITLE OF INVENTION: Proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 538
; LENGTH: 4316
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)

```


